

(2) INFORMATION FOR SEQ ID NO:1170:

- SEQUENCE CHARACTERISTICS
- (A) LENGTH: 870 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..870

- (D) OTHER INFORMATION: / Ceres Seq. ID 1597162

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1170:

(2) INFORMATION FOR SEQ ID NO:1171:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..289

- (D) OTHER INFORMATION: / Ceres Seq. ID 1597163

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1171:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.11/1.															
Met	Ala	Thr	Leu	Phe	Thr	Ala	Thr	Val	Pro	Ser	His	His	Arg	Phe	Val
1				5					10					15	
Ser	Pro	Ser	Gln	His	Pro	Lys	Gln	Ser	Leu	Leu	Ser	Gln	Ser	Leu	Ser
			20					25					30		
Val	Thr	Phe	Thr	Glu	Asn	Pro	Gln	Pro	Thr	Ala	Val	Val	Thr	Leu	Gln
		35					40					45			
Glu	Gln	Gln	Leu	Thr	Asp	Trp	Ile	Thr	Ser	Pro	Val	Thr	Arg	Arg	Phe
	50					55					60				
Gly	Ile	Gly	Ala	Gly	Phe	Thr	Trp	Ala	Gly	Phe	Leu	Ala	Phe	Gly	Val
65					70					75					80
Val	Ser	Glu	Gln	Met	Lys	Lys	Ser	Arg	Leu	Asp	Val	Phe	Gln	Glu	Glu
				85					90					95	
Asp	Asn	Thr	Arg	Gly	Leu	Glu	Lys	Gln	Glu	Glu	Ile	Ile	Leu	Pro	Asn
			100					105					110		
Gly	Ile	Arg	Tyr	Tyr	Asp	Leu	Gln	Val	Gly	Ser	Gly	Ala	Thr	Pro	Ser
		115					120					125			
Ser	Gly	Tyr	Leu	Val	Val	Phe	Asp	Val	Lys	Gly	Gln	Val	His	Gly	Thr
	130					135					140				

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(2) INFORMATION FOR SEQ ID NO:1172:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 205 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: peptide
      (ix) FEATURE:
            (A) NAME/KEY: peptide
            (B) LOCATION: 1..205
            (D) OTHER INFORMATION: / Ceres Seq. ID 1597165
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1172:
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(2) INFORMATION FOR SEQ ID NO:1173:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 600 base pairs

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.1175.							
atggggaag	gtaaccagtt	ggaagaagtc	agctacatca	acaacaacca	gggtggctac		60
aaaggataca	acaacttcaa	aaccaacaat	cccaacctct	cctaccgtag	caccagcggt		120
gctaattctc	aggatcaggt	gtatcccggt	caacaacaac	aaggtcagaa	caaacctttt		180
gttctctaca	accaaggttt	ctgtcttaag	cagcaatttn	tggggaacta	ccagccgcca		240
ccaccactcg	gatttgaca	tcagcaaaac	catgatggaa	acactgaata	ccaaagtccg		300
atacttagag	ggacattctg	catcttcttc	agctccaaca	caaacaagcc	aaactacca		360
ggcaaagcag	ttcagaatct	aaaagaatat	gctcatgcta	ttacactgcg	tagtggaaaa		420
gcacttccaa	ctagggagga	accaaagacg	gtcactgagg	acagtgaaga	tcaagatgga		480
gaggatttaa	gtctcgagca	accactcgac	ntgtcactcg	agcancact	cgaccaacca		540
ctcgagcaac	cactcgaccg	tgctactcaa	cctatcttcc	cagcagtatc	atcaacgtag		600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1174:

(A) LENGTH: 126 amino acids

Variable	Mean	SD	Min	Max
Age	38.5	12.5	25	65
Gender	0.5	0.5	0	1
Marital status	0.5	0.5	0	1
Education	12.5	2.5	9	16
Income	3500	1500	1000	8000
Health status	0.5	0.5	0	1
Exercise frequency	0.5	0.5	0	1
Stress level	0.5	0.5	0	1
Sleep quality	0.5	0.5	0	1
Work satisfaction	0.5	0.5	0	1
Life satisfaction	0.5	0.5	0	1
Depression score	10	10	0	40
Anxiety score	10	10	0	40
Quality of life score	10	10	0	40

- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..126  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597173  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1175:

Trp	Gly	Arg	Val	Thr	Ser	Trp	Lys	Lys	Ser	Ala	Thr	Ser	Thr	Thr	Thr
1				5				10						15	
Arg	Val	Ala	Thr	Lys	Asp	Thr	Thr	Thr	Ser	Lys	Pro	Thr	Ile	Pro	Thr
			20					25					30		
Ser	Pro	Thr	Val	Ala	Pro	Ala	Leu	Leu	Ile	Leu	Arg	Ile	Arg	Cys	Ile
		35					40					45			
Pro	Cys	Asn	Asn	Asn	Lys	Val	Arg	Thr	Asn	Leu	Leu	Phe	Ser	Thr	Thr
	50				55					60					
Lys	Val	Ser	Phe	Leu	Ser	Ser	Asn	Xaa	Trp	Gly	Thr	Thr	Ser	Arg	His
65				70				75						80	
His	His	Leu	Asp	Leu	His	Ile	Ser	Lys	Thr	Met	Met	Glu	Thr	Leu	Asn
			85					90						95	
Thr	Lys	Val	Arg	Tyr	Leu	Glu	Gly	His	Ser	Ala	Ser	Ser	Ser	Ala	Pro
			100				105						110		
Thr	Gln	Thr	Ser	Gln	Thr	Thr	Gln	Ala	Lys	Gln	Phe	Arg	Ile		
	115						120						125		

(2) INFORMATION FOR SEQ ID NO:1176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1026  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1176:

gaagaacccc	gtaacgttta	tctcgggttg	tgtctctgatg	ggttcaatcc	atttggcatg	60
tctcgtaatc	attcgttgtg	gcctgtgatc	ctaactcctt	ataattttacc	ccctgggtatg	120
tgcattgaata	cagagtactt	atttcttacc	attctgaatt	ctgggtccaaa	tcatcctcga	180
gctagtcttg	atgtcttcct	ccaacctctt	attgaggagt	taaaagagtt	gtgggtctact	240
ggagtcgatg	cgtacgatgt	ttcattgagt	cagaatttta	atctaaaagc	agtactacta	300
tggacgatta	gcgactttcc	ggcgtatagc	atgttatcag	gatggactac	tcagttttgt	360
aaatgtagta	tgttcgaaga	ttatctttct	gcgaaatc	catgcttgcc	cgaaaaagaa	420
ctctacgcga	gaagagcgaa	agaatatcat	ctatgggtta	aagaatatgt	aacatactgg	480
aacactactt	ctccatttcc	tacttgggtt	caagagattg	tgcaaggacc	tttgaacaag	540
gttaaaactt	ggccaatgta	tttcacaaga	ggatatttgt	ttcatacgca	aaatcacggc	600
gctggacgaa	agacatgtaa	ctatgggggtc	tgtgtttaaag	gtggaaatta	cgctgattca	660
tctgatgaag	cggattttcta	cggtacctta	actgataata	tagaactcga	gtatgaggat	720
caagtttgtt	atattccgta	tccatatacg	aagaaaccaa	agaacatttg	gctcaatggt	780
ctaaaagtca	atccgagggg	aaatatttct	ggagaatatg	aaaacaatga	tccaactctt	840
ttgcaaacag	aaaatgatga	tgatgttttg	ctcactacaa	ttgaagatct	tgttcttgaa	900
actccggtag	ccaacttaaa	cccaataatc	cttgattacg	atgtcgggga	tgctgaacca	960
gaagacgaat	tccgatgtaa	tttatcgtcc	tcggacgaag	atgaagtaga	agatgaagat	1020
gtataa						

(2) INFORMATION FOR SEQ ID NO:1177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

00669930-101300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1177:

(2) INFORMATION FOR SEQ ID NO:1178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 322 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..322

(D) OTHER INFORMATION: / Ceres Seq. ID 1597194

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1178:

Met Ser Arg Asn His Ser Leu Trp Pro Val Ile Leu Thr Pro Tyr Asn  
1 5 10 15  
Leu Pro Pro Gly Met Cys Met Asn Thr Glu Tyr Leu Phe Leu Thr Ile  
20 25 30  
Leu Asn Ser Gly Pro Asn His Pro Arg Ala Ser Leu Asp Val Phe Leu  
35 40 45  
Gln Pro Leu Ile Glu Glu Leu Lys Glu Leu Trp Ser Thr Gly Val Asp  
50 55 60  
Ala Tyr Asp Val Ser Leu Ser Gln Asn Phe Asn Leu Lys Ala Val Leu  
65 70 75 80  
Leu Trp Thr Ile Ser Asp Phe Pro Ala Tyr Ser Met Leu Ser Gly Trp  
85 90 95  
Thr Thr Gln Phe Cys Lys Cys Ser Met Phe Glu Asp Tyr Leu Ser Ala  
100 105 110  
Lys Tyr Pro Cys Leu Pro Glu Lys Glu Leu Tyr Ala Arg Arg Ala Lys  
115 120 125  
Glu Tyr His Leu Trp Val Lys Glu Tyr Val Thr Tyr Trp Asn Thr Thr  
130 135 140  
Ser Pro Phe Pro Thr Trp Val Gln Glu Ile Val Gln Gly Pro Leu Asn  
145 150 155 160  
Lys Val Lys Thr Trp Pro Met Tyr Phe Thr Arg Gly Tyr Leu Phe His  
165 170 175  
Thr Gln Asn His Gly Ala Gly Arg Lys Thr Cys Asn Tyr Gly Val Cys  
180 185 190  
Val Lys Gly Gly Asn Tyr Ala Asp Ser Ser Asp Glu Ala Asp Phe Tyr  
195 200 205  
Gly Thr Leu Thr Asp Asn Ile Glu Leu Glu Tyr Glu Asp Gln Val Cys  
210 215 220  
Tyr Ile Pro Tyr Pro Tyr Thr Lys Lys Pro Lys Asn Ile Trp Leu Asn  
225 230 235 240  
Val Leu Lys Val Asn Pro Arg Gly Asn Ile Ser Gly Glu Tyr Glu Asn  
245 250 255  
Asn Asp Pro Thr Leu Leu Gln Thr Glu Asn Asp Asp Asp Val Leu Leu  
260 265 270  
Thr Thr Ile Glu Asp Leu Val Leu Glu Thr Pro Val Ala Asn Leu Asn  
275 280 285  
Pro Ile Ile Leu Asp Tyr Asp Val Gly Asp Ala Glu Pro Glu Asp Glu  
290 295 300  
Phe Arg Cys Asn Leu Ser Ser Ser Asp Glu Asp Glu Val Glu Asp Glu  
305 310 315 320  
Asp Val

(2) INFORMATION FOR SEQ ID NO:1179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..302
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1179:

Met Cys Met Asn Thr Glu Tyr Leu Phe Leu Thr Ile Leu Asn Ser Gly  
1 5 10 15  
Pro Asn His Pro Arg Ala Ser Leu Asp Val Phe Leu Gln Pro Leu Ile  
20 25 30  
Glu Glu Leu Lys Glu Leu Trp Ser Thr Gly Val Asp Ala Tyr Asp Val  
35 40 45

00000000 00000000

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1180:

60  
120  
180  
240

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1181:

Ser	Ser	Glu	Val	Ser	Pro	Val	Val	Leu	Met	Gly	Asn	Arg	Leu	Thr	Gln
1				5					10					15	
Leu	Leu	Asp	Ala	Met	Glu	Leu	Ser	Arg	Gln	Thr	Met	Lys	Thr	Val	Lys
			20					25					30		
Gln	Asn	Leu	Trp	Trp	Ala	Phe	Gly	Tyr	Asn	Ile	Val	Gly	Ile	Pro	Ile
		35					40					45			
Ala	Ala	Gly	Val	Leu	Leu	Pro	Leu	Thr	Gly	Thr	Met	Leu	Thr	Pro	Ser
	50					55					60				
Met	Ala	Gly	Ala	Leu	Met	Xaa	Cys	Lys	Leu	Ser	Arg	Cys	His	Asp	
65					70					75					

(2) INFORMATION FOR SEQ ID NO:1182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:
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- ERROR KEY:
- (A) NAME/KEY: peptide
  - (B) LOCATION: 1..70
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1597210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1182:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:
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- (A) NAME/KEY: peptide  
(B) LOCATION: 1..59  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1183:

(x1) SEQUENCE DESCRIPTION: Cg2															
Met	Glu	Leu	Ser	Arg	Gln	Thr	Met	Lys	Thr	Val	Lys	Gln	Asn	Leu	Trp
1				5					10					15	
Trp	Ala	Phe	Gly	Tyr	Asn	Ile	Val	Gly	Ile	Pro	Ile	Ala	Ala	Gly	Val
			20					25					30		
Leu	Leu	Pro	Leu	Thr	Gly	Thr	Met	Leu	Thr	Pro	Ser	Met	Ala	Gly	Ala
		35					40					45			
Leu	Met	Xaa	Cys	Lys	Leu	Ser	Arg	Cys	His	Asp					
	50					55									

(2) INFORMATION FOR SEQ ID NO:1184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 982 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -



(D) OTHER INFORMATION: / Ceres Seq. ID 1597224

aacacaattt	gatacgcgtc	agtttgacca	gaggctgaat	gaagttctcg	atggacagga	60
tgagttcttc	acctcatatg	atgaggtcca	tgagagcttt	gatgccatgg	gtttgcaaga	120
gaatcttctt	aggggtatct	atgcttacgg	tttcgaaaag	ccttctgcta	ttcagcaaag	180
aggaattgta	cccttttgca	agggctctga	tgtgatccag	caggcacagt	ctgggtactgg	240
aaaaaccgcc	actttctgct	ctgggtgtctt	gcagcagctt	gaatatgcc	ttctccagtg	300
ccaggctctc	gttttggctc	ccaccagaga	gcttgctcag	cagattgaga	aggctatgctg	360
tgcccttggt	gactaccaag	gtgtcaagg	tcatgctgt	gttggtgga	ccagtgctcg	420
tnaggatcag	cgcattctcc	aggtcgggt	tcatgttgtc	gttggaactc	ctgggtcgtgt	480
ttttgacatg	cttagaagac	aatctctccg	ccctgactgc	atcaagatgt	ttgtccttga	540
tgaagctgat	gaaatgctct	cccgtggttt	caaggatcag	atctatgaca	tattccagct	600
tctccacca	aagattcagg	ttggagtgtt	ctctgcgaca	atgcctccgg	aagctttgga	660
gatcacaagg	aaattcatga	gcaaaccagt	gagaatcttg	gtgaaacgtg	atgagctcac	720
acttgaaggn	tatcaagcaa	ttctacgtga	ancgtggaga	aagaagactg	gaangcttga	780
gactctctgc	gatctctacg	nagactctag	ccatcactca	gagtgtcatc	tttgtcaaca	840
ctcgtcgcaa	ggtcganctg	gctncacaga	caaaatgaga	agccgtgacc	acacagctctc	900
agcnnnctca	tgagacatg	gaccaaaaca	ccagagacat	catcatgaga	gagttcagggt	960
cntgctcgt	ctcgtgttct	aa				

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..326

(D) OTHER INFORMATION: / Ceres Seq. ID 1597225

Thr 1	Gln	Phe	Asp	Thr 5	Arg	Gln	Phe	Asp	Gln 10	Arg	Leu	Asn	Glu 15	Val	Leu
Asp	Gly	Gln	Asp 20	Glu	Phe	Phe	Thr	Ser 25	Tyr	Asp	Glu	Val 30	His	Glu	Ser
Phe	Asp	Ala 35	Met	Gly	Leu	Gln	Glu 40	Asn	Leu	Leu	Arg	Gly 45	Ile	Tyr	Ala
Tyr	Gly 50	Phe	Glu	Lys	Pro	Ser 55	Ala	Ile	Gln	Gln	Arg 60	Gly	Ile	Val	Pro
Phe 65	Cys	Lys	Gly	Leu	Asp 70	Val	Ile	Gln	Gln	Ala 75	Gln	Ser	Gly	Thr	Gly 80
Lys	Thr	Ala	Thr	Phe 85	Cys	Ser	Gly	Val	Leu 90	Gln	Gln	Leu	Asp 95	Tyr	Ala
Leu	Leu	Gln	Cys 100	Gln	Ala	Leu	Val	Leu 105	Ala	Pro	Thr	Arg	Glu 110	Leu	Ala
Gln	Gln	Ile 115	Glu	Lys	Val	Met	Arg 120	Ala	Leu	Gly	Asp	Tyr 125	Gln	Gly	Val
Lys	Val 130	His	Ala	Cys	Val	Gly 135	Gly	Thr	Ser	Val	Arg 140	Xaa	Asp	Gln	Arg
Ile 145	Leu	Gln	Ala	Gly	Val 150	His	Val	Val	Val	Gly 155	Thr	Pro	Gly	Arg	Val 160
Phe	Asp	Met	Leu	Arg 165	Arg	Gln	Ser	Leu	Arg 170	Pro	Asp	Cys	Ile	Lys 175	Met
Phe	Val	Leu	Asp 180	Glu	Ala	Asp	Glu	Met 185	Leu	Ser	Arg	Gly 190	Phe	Lys	Asp
Gln	Ile 195	Tyr	Asp	Ile	Phe	Gln	Leu 200	Leu	Pro	Pro	Lys	Ile 205	Gln	Val	Gly
Val	Phe 210	Ser	Ala	Thr	Met	Pro	Pro 215	Glu	Ala	Leu	Glu 220	Ile	Thr	Arg	Lys
Phe	Met	Ser	Lys	Pro	Val	Arg	Ile	Leu	Val	Lys	Arg	Asp	Glu	Leu	Thr

[illegible]

225		230		235		240									
Leu	Glu	Xaa	Tyr	Gln	Ala	Ile	Leu	Arg	Glu	Xaa	Trp	Arg	Lys	Lys	Thr
		245		250		255									
Gly	Xaa	Leu	Glu	Thr	Leu	Cys	Asp	Leu	Tyr	Xaa	Asp	Ser	Ser	His	His
		260		265		270									
Ser	Glu	Cys	His	Leu	Cys	Gln	His	Ser	Ser	Gln	Gly	Arg	Xaa	Gly	Xaa
		275		280		285									
Thr	Asp	Lys	Met	Arg	Ser	Arg	Asp	His	Thr	Val	Ser	Xaa	Xaa	Ser	Trp
		290		295		300									
Arg	His	Gly	Pro	Lys	His	Gln	Arg	His	His	His	Glu	Arg	Val	Gln	Val
305				310		315									320
Xaa	Ala	Arg	Leu	Val	Phe										
		325													

(2) INFORMATION FOR SEQ ID NO:1186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..291
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1186:

Met	Gly	Leu	Gln	Glu	Asn	Leu	Leu	Arg	Gly	Ile	Tyr	Ala	Tyr	Gly	Phe
1			5						10					15	
Glu	Lys	Pro	Ser	Ala	Ile	Gln	Gln	Arg	Gly	Ile	Val	Pro	Phe	Cys	Lys
		20						25				30			
Gly	Leu	Asp	Val	Ile	Gln	Gln	Ala	Gln	Ser	Gly	Thr	Gly	Lys	Thr	Ala
		35					40					45			
Thr	Phe	Cys	Ser	Gly	Val	Leu	Gln	Gln	Leu	Asp	Tyr	Ala	Leu	Leu	Gln
	50					55				60					
Cys	Gln	Ala	Leu	Val	Leu	Ala	Pro	Thr	Arg	Glu	Leu	Ala	Gln	Gln	Ile
65				70					75					80	
Glu	Lys	Val	Met	Arg	Ala	Leu	Gly	Asp	Tyr	Gln	Gly	Val	Lys	Val	His
			85						90				95		
Ala	Cys	Val	Gly	Thr	Ser	Val	Arg	Xaa	Asp	Gln	Arg	Ile	Leu	Gln	
		100					105					110			
Ala	Gly	Val	His	Val	Val	Val	Gly	Thr	Pro	Gly	Arg	Val	Phe	Asp	Met
		115					120					125			
Leu	Arg	Arg	Gln	Ser	Leu	Arg	Pro	Asp	Cys	Ile	Lys	Met	Phe	Val	Leu
		130				135					140				
Asp	Glu	Ala	Asp	Glu	Met	Leu	Ser	Arg	Gly	Phe	Lys	Asp	Gln	Ile	Tyr
145				150					155					160	
Asp	Ile	Phe	Gln	Leu	Pro	Pro	Lys	Ile	Gln	Val	Gly	Val	Phe	Ser	
			165					170					175		
Ala	Thr	Met	Pro	Pro	Glu	Ala	Leu	Glu	Ile	Thr	Arg	Lys	Phe	Met	Ser
		180					185						190		
Lys	Pro	Val	Arg	Ile	Leu	Val	Lys	Arg	Asp	Glu	Leu	Thr	Leu	Glu	Xaa
		195					200					205			
Tyr	Gln	Ala	Ile	Leu	Arg	Glu	Xaa	Trp	Arg	Lys	Lys	Thr	Gly	Xaa	Leu
	210					215					220				
Glu	Thr	Leu	Cys	Asp	Leu	Tyr	Xaa	Asp	Ser	Ser	His	His	Ser	Glu	Cys
225					230				235					240	
His	Leu	Cys	Gln	His	Ser	Ser	Gln	Gly	Arg	Xaa	Gly	Xaa	Thr	Asp	Lys
			245					250						255	
Met	Arg	Ser	Arg	Asp	His	Thr	Val	Ser	Xaa	Xaa	Ser	Trp	Arg	His	Gly
		260					265						270		
Pro	Lys	His	Gln	Arg	His	His	His	Glu	Arg	Val	Gln	Val	Xaa	Ala	Arg
		275					280						285		

00669930 "101300

(2) INFORMATION FOR SEQ ID NO:1187:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..208

(D) OTHER INFORMATION: / Ceres Seq. ID 1597227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1187:

(2) INFORMATION FOR SEQ ID NO:1188:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..342

(D) OTHER INFORMATION: / Ceres Seq. ID 1597228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1188:

atgaagtttg	acatcagaga	agcttcaggg	aatcaacaa	caggagttca	gaacatnaat	60
attgatgaag	nngcagaagc	tggaacccca	ccaagagtta	actatacttc	tcaacttagc	120
aagctgaaga	ggacttttga	ccacaagaag	agagcaacag	aaaggctagc	tcagactgga	180
gatcctacaa	aagatgactg	ctctgtaaga	gtcaagctta	gtgaattaaa	acaagctcac	240
ttggggaggaa	gtccccatgtc	tatccaggnt	tgtctacttg	atcattataa	agtcaattggt	300
cagatnaact	caaaccaagt	caagaaagat	ctcagccgtt	ga		

(2) INFORMATION FOR SEQ ID NO:1189:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 113 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..113  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1597229  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1189:  
Met Lys Phe Asp Ile Arg Glu Ala Ser Gly Lys Ser Thr Thr Gly Val  
1                  5                  10                  15  
Gln Asn Xaa Asn Ile Asp Glu Xaa Ala Glu Ala Gly Thr Pro Pro Arg  
                  20                  25                  30  
Val Asn Tyr Thr Ser Gln Leu Ser Lys Leu Lys Arg Thr Phe Asp His  
                  35                  40                  45  
Lys Lys Arg Ala Thr Glu Arg Leu Ala Gln Thr Gly Asp Pro Thr Lys  
                  50                  55                  60  
Asp Asp Cys Ser Val Arg Val Lys Leu Ser Glu Leu Lys Gln Ala His  
65                  70                  75                  80  
Leu Gly Gly Ser Pro Met Ser Ile Gln Xaa Cys Leu Ile Asp His Tyr  
                  85                  90                  95  
Lys Val Asn Gly Arg Xaa Asn Ser Asn Gln Val Lys Lys Asp Leu Ser  
                  100                  105                  110  
Arg

(2) INFORMATION FOR SEQ ID NO:1190:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1032 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1032

(D) OTHER INFORMATION: / Ceres Seq. ID 1597257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1190:

atngcntgtn atcattnctg cttngtcatn cactngcctg ctatngccat ttctgctttt 60  
agtttcattt catttcgggtt attgcatact aggactgtta gaaccaacca actttctact 120  
tggtttgact tagagctttc tgatcatatc tcatctgttt gcgtcacact gaattggatt 180  
gacatcctaa aatactacaa cgacaggata gtaccttgca acctgcttta cagacgcac 240  
tctgattcgt ctgttatagc ccongctgct atctgttgca tgcatacacg gtcagaagga 300  
aatcagaacc tcctattcaa cgataacatc gaccgtattg ctgcgcaact aagagaacag 360  
acagaaaccg acacaatggc tgacgttgta gatgagcaag agcaacctac caacattggt 420  
gctggtgact tccctcacia ccacaaccag cgtcattggaa ttgttccacc tccagtacag 480  
aacaacaact ttgagatcaa aagcgggtctc attgctatgg ttcaaggga caagtttcat 540  
ggcctgccaa tggaggatcc gctagatcat ctngacgagt tngaaagnct ctgtgncctn 600  
actaaaatca atggagttag tgaagatggg ttnnnanttc gcttgtttcc attctcactt 660  
ggagataaag cccatctgtg ggaaaagacg ctaccccaga attcaatcac aacctgggat 720  
gactgcaaaa aggccttctt ggcaaaattc ttttccaact ccagaactgc aagactccgg 780  
aatgagatat ccgattttac tcagaagcaa aatgaaagct tctgtgaagc ttgggagcgc 840  
ttaagggtt atcaaacc aa atgccctcat cagcgattta agcangctnc tctnctcagc 900  
acactctata gagncgtctn gcctaagata aggatactgc ttgacaccgc ttcaaattggg 960  
aattttttga agaaggatgt tgaagaagga tggtagctag tngaaaanct ttgctcagtc 1020  
gnatggcaat na

(2) INFORMATION FOR SEQ ID NO:1191:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 343 amino acids  
    (B) TYPE: amino acid

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- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..343  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1597258  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1191:

Xaa Xaa Cys Xaa His Xaa Cys Xaa Val Xaa His Xaa Pro Ala Xaa Ala  
1 5 10 15  
Ile Ser Ala Phe Ser Phe Ile Ser Phe Arg Leu Leu His Thr Arg Thr  
20 25 30  
Val Arg Thr Asn Gln Leu Ser Thr Trp Leu Asp Leu Glu Leu Ser Asp  
35 40 45  
His Ile Ser Ser Val Cys Val Thr Leu Asn Trp Ile Asp Ile Leu Lys  
50 55 60  
Tyr Tyr Asn Asp Arg Ile Val Pro Cys Asn Leu Leu Tyr Arg Arg Ile  
65 70 75 80  
Ser Asp Ser Ser Val Ile Ala Xaa Ala Ala Ile Cys Cys Met His Thr  
85 90 95  
Arg Ser Glu Gly Asn Gln Asn Leu Leu Phe Asn Asp Asn Ile Asp Arg  
100 105 110  
Ile Ala Arg Gln Leu Arg Glu Gln Thr Glu Thr Asp Thr Met Ala Asp  
115 120 125  
Val Val Asp Glu Gln Glu Gln Pro Thr Asn Ile Gly Ala Gly Asp Phe  
130 135 140  
Pro His Asn His Asn Gln Arg His Gly Ile Val Pro Pro Pro Val Gln  
145 150 155 160  
Asn Asn Asn Phe Glu Ile Lys Ser Gly Leu Ile Ala Met Val Gln Gly  
165 170 175  
Asn Lys Phe His Gly Leu Pro Met Glu Asp Pro Leu Asp His Xaa Asp  
180 185 190  
Glu Xaa Glu Xaa Leu Cys Xaa Xaa Thr Lys Ile Asn Gly Val Ser Glu  
195 200 205  
Asp Gly Xaa Xaa Xaa Arg Leu Phe Pro Phe Ser Leu Gly Asp Lys Ala  
210 215 220  
His Leu Trp Glu Lys Thr Leu Pro Gln Asn Ser Ile Thr Thr Trp Asp  
225 230 235 240  
Asp Cys Lys Lys Ala Phe Leu Ala Lys Phe Phe Ser Asn Ser Arg Thr  
245 250 255  
Ala Arg Leu Arg Asn Glu Ile Ser Gly Phe Thr Gln Lys Gln Asn Glu  
260 265 270  
Ser Phe Cys Glu Ala Trp Glu Arg Phe Lys Gly Tyr Gln Thr Lys Cys  
275 280 285  
Pro His His Gly Phe Lys Xaa Ala Xaa Xaa Leu Ser Thr Leu Tyr Arg  
290 295 300  
Xaa Val Xaa Pro Lys Ile Arg Ile Leu Leu Asp Thr Ala Ser Asn Gly  
305 310 315 320  
Asn Phe Leu Lys Lys Asp Val Glu Glu Gly Trp Xaa Leu Xaa Glu Xaa  
325 330 335  
Leu Cys Ser Val Xaa Trp Gln  
340

- (2) INFORMATION FOR SEQ ID NO:1192:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 250 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide

00669980-101300

(B) LOCATION: 1..250

(D) OTHER INFORMATION: / Ceres Seq. ID 1597259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1192:

Met His Thr Arg Ser Glu Gly Asn Gln Leu Leu Phe Asn Asp Asn  
1 5 10 15  
Ile Asp Arg Ile Ala Arg Gln Leu Arg Glu Gln Thr Glu Thr Asp Thr  
20 25 30  
Met Ala Asp Val Val Asp Glu Gln Glu Gln Pro Thr Asn Ile Gly Ala  
35 40 45  
Gly Asp Phe Pro His Asn His Asn Gln Arg His Gly Ile Val Pro Pro  
50 55 60  
Pro Val Gln Asn Asn Asn Phe Glu Ile Lys Ser Gly Leu Ile Ala Met  
65 70 75 80  
Val Gln Gly Asn Lys Phe His Gly Leu Pro Met Glu Asp Pro Leu Asp  
85 90 95  
His Xaa Asp Glu Xaa Glu Xaa Leu Cys Xaa Xaa Thr Lys Ile Asn Gly  
100 105 110  
Val Ser Glu Asp Gly Xaa Xaa Xaa Arg Leu Phe Pro Phe Ser Leu Gly  
115 120 125  
Asp Lys Ala His Leu Trp Glu Lys Thr Leu Pro Gln Asn Ser Ile Thr  
130 135 140  
Thr Trp Asp Asp Cys Lys Lys Ala Phe Leu Ala Lys Phe Phe Ser Asn  
145 150 155 160  
Ser Arg Thr Ala Arg Leu Arg Asn Glu Ile Ser Gly Phe Thr Gln Lys  
165 170 175  
Gln Asn Glu Ser Phe Cys Glu Ala Trp Glu Arg Phe Lys Gly Tyr Gln  
180 185 190  
Thr Lys Cys Pro His His Gly Phe Lys Xaa Ala Xaa Xaa Leu Ser Thr  
195 200 205  
Leu Tyr Arg Xaa Val Xaa Pro Lys Ile Arg Ile Leu Leu Asp Thr Ala  
210 215 220  
Ser Asn Gly Asn Phe Leu Lys Lys Asp Val Glu Glu Gly Trp Xaa Leu  
225 230 235 240  
Xaa Glu Xaa Leu Cys Ser Val Xaa Trp Gln  
245 250

(2) INFORMATION FOR SEQ ID NO:1193:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..218

(D) OTHER INFORMATION: / Ceres Seq. ID 1597260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1193:

Met Ala Asp Val Val Asp Glu Gln Glu Gln Pro Thr Asn Ile Gly Ala  
1 5 10 15  
Gly Asp Phe Pro His Asn His Asn Gln Arg His Gly Ile Val Pro Pro  
20 25 30  
Pro Val Gln Asn Asn Asn Phe Glu Ile Lys Ser Gly Leu Ile Ala Met  
35 40 45  
Val Gln Gly Asn Lys Phe His Gly Leu Pro Met Glu Asp Pro Leu Asp  
50 55 60  
His Xaa Asp Glu Xaa Glu Xaa Leu Cys Xaa Xaa Thr Lys Ile Asn Gly  
65 70 75 80  
Val Ser Glu Asp Gly Xaa Xaa Xaa Arg Leu Phe Pro Phe Ser Leu Gly  
85 90 95  
Asp Lys Ala His Leu Trp Glu Lys Thr Leu Pro Gln Asn Ser Ile Thr  
100 105 110

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Thr Trp Asp Asp Cys Lys Lys Ala Phe Leu Ala Lys Phe Phe Ser Asn  
115 120 125  
Ser Arg Thr Ala Arg Leu Arg Asn Glu Ile Ser Gly Phe Thr Gln Lys  
130 135 140  
Gln Asn Glu Ser Phe Cys Glu Ala Trp Glu Arg Phe Lys Gly Tyr Gln  
145 150 155 160  
Thr Lys Cys Pro His His Gly Phe Lys Xaa Ala Xaa Xaa Leu Ser Thr  
165 170 175  
Leu Tyr Arg Xaa Val Xaa Pro Lys Ile Arg Ile Leu Leu Asp Thr Ala  
180 185 190  
Ser Asn Gly Asn Phe Leu Lys Lys Asp Val Glu Glu Gly Trp Xaa Leu  
195 200 205  
Xaa Glu Xaa Leu Cys Ser Val Xaa Trp Gln  
210 215

(2) INFORMATION FOR SEQ ID NO:1194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..591
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1194:

atgtcaacaa gatcgccact cgcaaggatt caacctacaa gaacgttggt tggacttccc	60
ngtggctaca aaggtcgcgga ctttntcat cgcnaggagac ctattccat ctctccngc	120
aattctcaag attctttgaa caaagatggt tgctttcacc ntggagtga cactactcgca	180
gctacttctc caaatgatac attttatgac ggaggatttc ctatgaaatc aggaacatca	240
atgtcgactc cttttgttgc aggaattgta gcactcctta agtctttgca ccctcattgg	300
tctccggccg ccattagatc tgctattggt actacagctt ggagaacaga tccatccgag	360
aaagccgcgga aaccgggtct tgtttacgat atgggagtta acgattatgt tctntatttg	420
tgctccgttg gttacacaga ttcattccatt actagacttg tccgcaagaa gacggtttgt	480
gcaaacccta aaccttcagt tcttgacctc aaattgcctt caatcacaat cccaaacctt	540
gcaaaaanga agttattatc actagaaccg ttaccaacgt tggaccagta g	

(2) INFORMATION FOR SEQ ID NO:1195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1195:

Met Ser Thr Arg Ser Pro Leu Ala Arg Ile Gln Pro Thr Arg Thr Leu  
1 5 10 15  
Val Gly Leu Pro Xaa Gly Tyr Lys Gly Arg Asp Phe Xaa His Arg Xaa  
20 25 30  
Gly Pro Ser Ser Ile Ser Pro Xaa Asn Ser Gln Asp Ser Leu Asn Lys  
35 40 45  
Asp Val Cys Phe His Xaa Gly Val Asn Ile Leu Ala Ala Thr Ser Pro  
50 55 60  
Asn Asp Thr Phe Tyr Asp Gly Gly Phe Pro Met Lys Ser Gly Thr Ser  
65 70 75 80  
Met Ser Thr Pro Phe Val Ala Gly Ile Val Ala Leu Leu Lys Ser Leu  
85 90 95  
His Pro His Trp Ser Pro Ala Ala Ile Arg Ser Ala Ile Val Thr Thr

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100 105 110  
Ala Trp Arg Thr Asp Pro Ser Glu Lys Ala Ala Lys Pro Gly Leu Val  
115 120 125  
Tyr Asp Met Gly Val Asn Asp Tyr Val Xaa Tyr Leu Cys Ser Val Gly  
130 135 140  
Tyr Thr Asp Ser Ser Ile Thr Arg Leu Val Arg Lys Lys Thr Val Cys  
145 150 155 160  
Ala Asn Pro Lys Pro Ser Val Leu Asp Leu Lys Leu Pro Ser Ile Thr  
165 170 175  
Ile Pro Asn Leu Ala Lys Xaa Lys Leu Leu Ser Leu Glu Pro Leu Pro  
180 185 190  
Thr Leu Asp Gln  
195

(2) INFORMATION FOR SEQ ID NO:1196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1597264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1196:

Met Lys Ser Gly Thr Ser Met Ser Thr Pro Phe Val Ala Gly Ile Val  
1 5 10 15  
Ala Leu Leu Lys Ser Leu His Pro His Trp Ser Pro Ala Ala Ile Arg  
20 25 30  
Ser Ala Ile Val Thr Thr Ala Trp Arg Thr Asp Pro Ser Glu Lys Ala  
35 40 45  
Ala Lys Pro Gly Leu Val Tyr Asp Met Gly Val Asn Asp Tyr Val Xaa  
50 55 60  
Tyr Leu Cys Ser Val Gly Tyr Thr Asp Ser Ser Ile Thr Arg Leu Val  
65 70 75 80  
Arg Lys Lys Thr Val Cys Ala Asn Pro Lys Pro Ser Val Leu Asp Leu  
85 90 95  
Lys Leu Pro Ser Ile Thr Ile Pro Asn Leu Ala Lys Xaa Lys Leu Leu  
100 105 110  
Ser Leu Glu Pro Leu Pro Thr Leu Asp Gln  
115 120

(2) INFORMATION FOR SEQ ID NO:1197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..714

(D) OTHER INFORMATION: / Ceres Seq. ID 1597281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1197:

tctgtctgtc tcgtcactca ggatcagatc ttagctaaat tgagacaagc tcaaaatgag 60  
taagcttcag agtgaggccg ttcgtgaagc catcactact atcacaggga aatccgaggc 120  
aaagaaacgt aactttgtcg agactattga gctccagatc ggtctgaaga actatgaccc 180  
tcaaaaggac aagcgtttca gtggatctgt caagttacca catatccccc gtcctaaaat 240  
gaagatctgc atgctcggag atgccagca tgttgaagag gaaaattccc aactcttgtg 300  
agccaccagg aatccttgga gtcaaagggtg aatgaaacaa aggcaacagt gaagttccag 360  
ctgaagaagg ttctgtgcat gggagttgca gttggtaacc tttcaatgga agagaagcag 420  
atctttcaga atgtgcagat gagcgtcaac ttctctgtct cgctattgaa gaagaactgg 480

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(2) INFORMATION FOR SEQ ID NO:1198:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1198:

(2) INFORMATION FOR SEQ ID NO:1199:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1199:

(2) INFORMATION FOR SEQ ID NO:1200:

- ```
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
```

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1200:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1200:  
Met Glu Glu Lys Gln Ile Phe Gln Asn Val Gln Met Ser Val Asn Phe

[illegible]

| SEQUENCE DESCRIPTION: SEQ ID NO:12345 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile                                   | Glu | Ser | Leu | Gly | Ser | Leu | Cys | Val | Cys | Lys | Ser | Asp | Ala | Glu | Tyr |
| 1                                     |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe                                   | Ala | Lys | Ala | Ala | Ala | Ser | Arg | Asp | Ser | Glu | Met | Ala | Thr | Glu | Asp |
|                                       |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val                                   | Gln | Asp | Pro | Arg | Ile | Ala | Lys | Ile | Ala | Ser | Ser | Ile | Arg | Val | Ile |
|                                       |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro                                   | Asp | Phe | Pro | Lys | Pro | Gly | Ile | Met | Phe | Gln | Asp | Ile | Thr | Thr | Leu |
|                                       | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu                                   | Leu | Asp | Thr | Glu | Ala | Phe | Lys | Asp | Thr | Ile | Ala | Leu | Phe | Val | Asp |
| 65                                    |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg                                   | Tyr | Lys | Asp | Lys | Gly | Ile | Ser | Val | Val | Ala | Gly | Val | Glu | Ala | Arg |
|                                       |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Gly                                   | Phe | Ile | Phe | Gly | Pro | Pro | Ile | Ala | Leu | Ala | Ile | Gly | Ala | Lys | Phe |
|                                       |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val                                   | Pro | Met | Arg | Thr | Pro | Lys | Lys | Leu | Pro | Gly | Lys | Val | Ile | Ser | Glu |
|                                       |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu                                   | Tyr | Ser | Leu | Glu | Tyr | Gly | Pro | Asp | Thr | Ile | Glu | Met | His | Val | Gly |
|                                       | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

Ala Val Glu Pro Gly Glu Arg Ala Ile Ile Ile Asp Xaa Leu Ile Ala  
145 150 155 160  
Thr Gly Gly Thr Leu Ala Ala Ala Ile Arg Leu Leu Glu Arg Val Gly  
165 170 175  
Val Xaa Ile Val Glu Cys Ala Cys Val Ile Glu Leu Pro Glu Leu Lys  
180 185 190  
Gly Lys Glu Lys Leu Gly Glu Thr Ser Leu Phe Val Leu Val Lys Ser  
195 200 205  
Ala Ala  
210

(2) INFORMATION FOR SEQ ID NO:1203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..183

(D) OTHER INFORMATION: / Ceres Seq. ID 1597287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1203:

Met Ala Thr Glu Asp Val Gln Asp Pro Arg Ile Ala Lys Ile Ala Ser  
1 5 10 15  
Ser Ile Arg Val Ile Pro Asp Phe Pro Lys Pro Gly Ile Met Phe Gln  
20 25 30  
Asp Ile Thr Thr Leu Leu Leu Asp Thr Glu Ala Phe Lys Asp Thr Ile  
35 40 45  
Ala Leu Phe Val Asp Arg Tyr Lys Asp Lys Gly Ile Ser Val Val Ala  
50 55 60  
Gly Val Glu Ala Arg Gly Phe Ile Phe Gly Pro Pro Ile Ala Leu Ala  
65 70 75 80  
Ile Gly Ala Lys Phe Val Pro Met Arg Thr Pro Lys Lys Leu Pro Gly  
85 90 95  
Lys Val Ile Ser Glu Glu Tyr Ser Leu Glu Tyr Gly Pro Asp Thr Ile  
100 105 110  
Glu Met His Val Gly Ala Val Glu Pro Gly Glu Arg Ala Ile Ile Ile  
115 120 125  
Asp Xaa Leu Ile Ala Thr Gly Gly Thr Leu Ala Ala Ala Ile Arg Leu  
130 135 140  
Leu Glu Arg Val Gly Val Xaa Ile Val Glu Cys Ala Cys Val Ile Glu  
145 150 155 160  
Leu Pro Glu Leu Lys Gly Lys Glu Lys Leu Gly Glu Thr Ser Leu Phe  
165 170 175  
Val Leu Val Lys Ser Ala Ala  
180

(2) INFORMATION FOR SEQ ID NO:1204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1597288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1204:

Met Phe Gln Asp Ile Thr Thr Leu Leu Leu Asp Thr Glu Ala Phe Lys  
1 5 10 15  
Asp Thr Ile Ala Leu Phe Val Asp Arg Tyr Lys Asp Lys Gly Ile Ser

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| (X1) SEQUENCE DESCRIPTION |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys                       | Leu | Gln | Ser |     | Glu | Ala | Val | Arg |     | Glu | Ala | Ile | Thr | Thr | Ile | Thr | Gly |
| 1                         |     |     |     | 5   |     |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys                       | Ser | Glu | Ala | Lys | Lys | Arg | Asn | Phe | Val | Glu | Thr | Ile | Glu | Leu | Gln |     |     |
|                           |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |     |
| Ile                       | Gly | Leu | Lys | Asn | Tyr | Asp | Pro | Gln | Lys | Asp | Lys | Arg | Phe | Ser | Gly |     |     |
|                           |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |     |
| Ser                       | Val | Lys | Leu | Pro | His | Ile | Pro | Arg | Pro | Lys | Met | Lys | Ile | Cys | Met |     |     |
|                           |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |     |
| Leu                       | Gly | Asp | Ala | Gln | His | Val | Glu | Glu | Asn | Met | Asp | Val | Glu | Ser | Leu |     |     |
| 65                        |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |     |
| Lys                       | Lys | Leu | Asn | Lys | Asn | Lys | Lys | Leu | Val | Lys | Lys | Leu | Ala | Lys | Lys |     |     |
|                           |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |     |
| Tyr                       | His | Ala | Phe | Leu | Ala | Ser | Glu | Ser | Val | Ile | Lys | Gln | Ile | Pro | Arg |     |     |

[illegible]

100 105 110  
Leu Leu Gly Pro Gly Leu Asn Lys Ala  
115 120

(2) INFORMATION FOR SEQ ID NO:1207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..62
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1207:

Met Lys Ile Cys Met Leu Gly Asp Ala Gln His Val Glu Glu Asn Met  
1 5 10 15  
Asp Val Glu Ser Leu Lys Lys Leu Asn Lys Asn Lys Lys Leu Val Lys  
20 25 30  
Lys Leu Ala Lys Lys Tyr His Ala Phe Leu Ala Ser Glu Ser Val Ile  
35 40 45  
Lys Gln Ile Pro Arg Leu Leu Gly Pro Gly Leu Asn Lys Ala  
50 55 60

(2) INFORMATION FOR SEQ ID NO:1208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1036 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1036
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1208:

acaatggatg agttataggt ttggttaaga cttgaaaagt cattgatcac ggcttttgtc 60  
cattattccg tgtttaaagt aatttacatt ctcttttaag atctctcagt ccaaagacaa 120  
tgcaaacaat aataatttct ccacttggtt ctcacgtctc ctgtcttgct cgtgctgttc 180  
cttgcaaccg tcttctcaac aaccaccacc gtgctcctcc ttcgatccgc ctctcaaacc 240  
accgttcaac cacctcactc cgctcttctt cctccgccgc agccagtcgg gacagtgaaa 300  
tggcgactga agatgtgcaa gatccagaa tcgctaagat tgcctcttcc attagagtca 360  
tccccgactt ccctaaacca ggaatcatgt ttcaggacat aacgacgctt cttctcgaca 420  
ctgaggcctt taaggatact attgctttgt ttgttgatag atacaaagat aaaggcatat 480  
ctgttggtgc aggtgttgaa gctagagggt tcatttttgg ccctcttatt gcgttggcta 540  
ttggtgcaa atttgttccc atgaggacgc ccaagaagct acctggaag gttatttcgg 600  
aggagtattc gttggagtat ggaccagata cgattgagat gcacgtaggt gcagtagagc 660  
ctggtgagcg tgctattatt attgatgncc tcattgccac ggggtgggact ctgctgctg 720  
caatccgact acttgaacga gtaggagtn agattgttga atgtgcttgc gtaattgagt 780  
taccagagct taagggaag gagaaactag gagagacgtc gctatttgtt cttgtaaagt 840  
cggctgctta acaagaaact ggaagtgaag gttattggat cgagtgttga tgctattttt 900  
catgtatggt gagacatttt gcgtgggatt tgatccttgt tgnttcaact tttatcatan 960  
ttggttcagn ctagaaaatg gcatttgaat gtcaggattc gattgcagtt tcctattgtt 1020  
ccacttaaaa tccccg

(2) INFORMATION FOR SEQ ID NO:1209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

09639930-101300

(A) NAME/KEY: peptide  
(B) LOCATION: 1..243  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1209:

Met Gln Thr Ile Ile Ile Ser Pro Leu Val Ser His Arg Leu Cys Leu  
1 5 10 15  
Ala Arg Ala Val Pro Cys Asn Arg Leu Leu Asn Asn His His Arg Ala  
20 25 30  
Pro Pro Ser Ile Arg Leu Ser Asn His Arg Ser Thr Thr Ser Leu Arg  
35 40 45  
Leu Phe Ser Ser Ala Ala Ala Ser Arg Asp Ser Glu Met Ala Thr Glu  
50 55 60  
Asp Val Gln Asp Pro Arg Ile Ala Lys Ile Ala Ser Ser Ile Arg Val  
65 70 75 80  
Ile Pro Asp Phe Pro Lys Pro Gly Ile Met Phe Gln Asp Ile Thr Thr  
85 90 95  
Leu Leu Leu Asp Thr Glu Ala Phe Lys Asp Thr Ile Ala Leu Phe Val  
100 105 110  
Asp Arg Tyr Lys Asp Lys Gly Ile Ser Val Val Ala Gly Val Glu Ala  
115 120 125  
Arg Gly Phe Ile Phe Gly Pro Pro Ile Ala Leu Ala Ile Gly Ala Lys  
130 135 140  
Phe Val Pro Met Arg Thr Pro Lys Lys Leu Pro Gly Lys Val Ile Ser  
145 150 155 160  
Glu Glu Tyr Ser Leu Glu Tyr Gly Pro Asp Thr Ile Glu Met His Val  
165 170 175  
Gly Ala Val Glu Pro Gly Glu Arg Ala Ile Ile Ile Asp Xaa Leu Ile  
180 185 190  
Ala Thr Gly Gly Thr Leu Ala Ala Ile Arg Leu Leu Glu Arg Val  
195 200 205  
Gly Val Xaa Ile Val Glu Cys Ala Cys Val Ile Glu Leu Pro Glu Leu  
210 215 220  
Lys Gly Lys Glu Lys Leu Gly Glu Thr Ser Leu Phe Val Leu Val Lys  
225 230 235 240  
Ser Ala Ala

(2) INFORMATION FOR SEQ ID NO:1210:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..183  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1210:

Met Ala Thr Glu Asp Val Gln Asp Pro Arg Ile Ala Lys Ile Ala Ser  
1 5 10 15  
Ser Ile Arg Val Ile Pro Asp Phe Pro Lys Pro Gly Ile Met Phe Gln  
20 25 30  
Asp Ile Thr Thr Leu Leu Leu Asp Thr Glu Ala Phe Lys Asp Thr Ile  
35 40 45  
Ala Leu Phe Val Asp Arg Tyr Lys Asp Lys Gly Ile Ser Val Val Ala  
50 55 60  
Gly Val Glu Ala Arg Gly Phe Ile Phe Gly Pro Pro Ile Ala Leu Ala  
65 70 75 80  
Ile Gly Ala Lys Phe Val Pro Met Arg Thr Pro Lys Lys Leu Pro Gly  
85 90 95  
Lys Val Ile Ser Glu Glu Tyr Ser Leu Glu Tyr Gly Pro Asp Thr Ile

09689980 "101300

| (X1) SEQUENCE DESCRIPTION: SEQ ID NO:1212 |            |            |            |             |             |  |  |     |
|-------------------------------------------|------------|------------|------------|-------------|-------------|--|--|-----|
| cacaatttga                                | tacgcgtcag | tttgaccaga | ggctgaatga | agttctcgat  | ggacagggatg |  |  | 60  |
| agttcttcac                                | ctcatatgat | gaggtccatg | agagctttga | tgccatgggt  | ttgcaagaga  |  |  | 120 |
| atcttcttag                                | gggtatctat | gcttacggtt | tcgaaaagcc | ttctgctatt  | cagcaaagag  |  |  | 180 |
| gaattgtacc                                | cttttgcaag | ggctcttgat | tgatccagca | ggcacagctct | ggtagctgaa  |  |  | 240 |
| aaaccgccac                                | tttctgctct | aggctcttgc | agcagcttga | cttagccctt  | ctccagtgcc  |  |  | 300 |
| aggctctcgt                                | tttggctccc | accagagagc | ttgctcagca | gattgagaag  | gtcatgcgtg  |  |  | 360 |

|            |            |             |            |            |            |      |
|------------|------------|-------------|------------|------------|------------|------|
| cccttggtga | ctaccaaggt | gtcaagggttc | atgcctgtgt | tggtggaacc | agtgtccgtn | 420  |
| aggatcagcg | cattctccag | gctgggtgttc | atgttgctgt | tggaactcct | ggtcgtgttt | 480  |
| ttgacatgct | tagaagacaa | tctctccgcc  | ctgactgcat | caagatgttt | gtccttgatg | 540  |
| aagctgatga | aatgctctcc | cgtgggtttca | aggatcagct | catggagaca | tggacaaaaa | 600  |
| caccagagac | atcatcatga | gagagttcag  | gtcntggctc | gtctcgtgtt | ctaatacaca | 660  |
| ccgatctctt | ggctcgtggt | atcgatgtgc  | agcaagtctc | tctagtcata | aanctttgac | 720  |
| ctcccaactc | agccagagaa | ttaccttcac  | cgtatcggaa | gaagtggaag | gttcgggaga | 780  |
| aagggtgtgg | cgattaactt | tgtgancnnt  | tgangatcag | agaatgctgt | ttgatattca | 840  |
| gaaantctnc | aatgtnggtt | gttgagnagc  | ttcccncaaa | cgtggctgat | ttngctgtga | 900  |
| agaagaagaa | gaagaagaan | gaagaaaggt  | tngcttgtn  | cgcnnntttc | ttatttngat | 960  |
| ttttgaccgc | tctnnnnntc | tctgaatcat  | cgatacatct | ttttcattct | ctagtattct | 1020 |
| tcatcaactc | tatcgaacat | atatatgtct  | cttctgacca | tatttctttt | ttatcaaagt | 1080 |
| caatatttat | ttcttct    |             |            |            |            |      |

(2) INFORMATION FOR SEQ ID NO:1213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..205
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1213:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Phe | Asp | Thr | Arg | Gln | Phe | Asp | Gln | Arg | Leu | Asn | Glu | Val | Leu | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Gln | Asp | Glu | Phe | Phe | Thr | Ser | Tyr | Asp | Glu | Val | His | Glu | Ser | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Ala | Met | Gly | Leu | Gln | Glu | Asn | Leu | Leu | Arg | Gly | Ile | Tyr | Ala | Tyr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Gly | Phe | Glu | Lys | Pro | Ser | Ala | Ile | Gln | Gln | Arg | Gly | Ile | Val | Pro | Phe |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Cys | Lys | Gly | Leu | Asp | Val | Ile | Gln | Gln | Ala | Gln | Ser | Gly | Thr | Gly | Lys |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Thr | Ala | Thr | Phe | Cys | Ser | Gly | Val | Leu | Gln | Leu | Asp | Tyr | Ala | Leu |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Leu | Gln | Cys | Gln | Ala | Leu | Val | Leu | Ala | Pro | Thr | Arg | Glu | Leu | Ala | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Ile | Glu | Lys | Val | Met | Arg | Ala | Leu | Gly | Asp | Tyr | Gln | Gly | Val | Lys |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | His | Ala | Cys | Val | Gly | Gly | Thr | Ser | Val | Arg | Xaa | Asp | Gln | Arg | Ile |
|     |     |     | 130 |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Leu | Gln | Ala | Gly | Val | His | Val | Val | Val | Gly | Thr | Pro | Gly | Arg | Val | Phe |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Asp | Met | Leu | Arg | Arg | Gln | Ser | Leu | Arg | Pro | Asp | Cys | Ile | Lys | Met | Phe |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Val | Leu | Asp | Glu | Ala | Asp | Glu | Met | Leu | Ser | Arg | Gly | Phe | Lys | Asp | Gln |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Leu | Met | Glu | Thr | Trp | Thr | Lys | Thr | Pro | Glu | Thr | Ser | Ser |     |     |     |
|     |     |     | 195 |     |     | 200 |     |     |     |     |     | 205 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..171

09669980-10300



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1214:

(2) INFORMATION FOR SEQ ID NO:1215:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1597347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1215:

(2) INFORMATION FOR SEQ ID NO:1216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1156 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

[illegible]

(D) OTHER INFORMATION: / Ceres Seq. ID 1597360

| (XI) SEQUENCE DESCRIPTION: SEQ ID NO:1101 |             |             |             |             |             |      |
|-------------------------------------------|-------------|-------------|-------------|-------------|-------------|------|
| tgtgcggctc                                | gaagaaggaa  | cggatgaagtc | tttaatatgaa | gaaaaaggag  | tgatcaaagg  | 60   |
| atgtacatac                                | aaaaataaag  | caggcggaaga | aacaacagcc  | ttggcacctc  | tcactgtagt  | 120  |
| atgcgcaggt                                | tgctactcaa  | accttcgtcg  | gtctctaaac  | gataacaatg  | ctgagggttct | 180  |
| gtcttaccaa                                | gttgcttaca  | tctcgaagaa  | ttgtcggctt  | gatgatccca  | aaaaccttca  | 240  |
| tttgataatg                                | tccaaaccct  | cctacatcat  | gttgtagcaa  | ttaagcagca  | ctgatgttcg  | 300  |
| ttgtggtttt                                | gaacttttct  | ccgccaaattt | tccttccatt  | gcaaaagggtg | aatgggttac  | 360  |
| ttttgcgaag                                | aacactctag  | ctcctcaggt  | acctccaaaa  | cttcgcaaaa  | tattcttgaa  | 420  |
| aggtctagat                                | gaaggagcac  | acataaaaagc | gggtgccagca | aagcgcatag  | cagcttcttt  | 480  |
| aaccaagaaa                                | aatggagtga  | ttgtgttggg  | agatgcattc  | aacatgcgtc  | atcnttcggg  | 540  |
| cgcggctggt                                | atgatggttt  | tattgtctga  | cattctcatt  | ctacgtcgtc  | ttctccagcc  | 600  |
| actaagcaac                                | cttgggtgatg | caaacaaagt  | ctcagaagtc  | attaagtcct  | ttaatattat  | 660  |
| ccgcaagcca                                | atgtcagcga  | cggatgaacac | attaggaaat  | gcattttctc  | aagttctaatt | 720  |
| tgcatcaact                                | gacgaagcaa  | aagaggcaat  | gagacaagggt | tgctatgatt  | acctctctag  | 780  |
| tggtggtttt                                | tgacgcgcg   | ggatgatggc  | tctactaggt  | ggcatgaatc  | ctcgtccgct  | 840  |
| ctctctcata                                | tatcatctat  | gtgctatcac  | tttacattca  | attggccatc  | ttctatctcc  | 900  |
| atttccttcc                                | ccccttagca  | tttggcatag  | cctcaggctt  | tttggtttgg  | ctttgaaaat  | 960  |
| gttggttccc                                | catctcaagg  | ctgagggagt  | tagcgaaatg  | ttttttccag  | caaacgcagc  | 1020 |
| cgcataatgc                                | aaaagctata  | tggccgcatac | tggtctttta  | acattgatgc  | tctaaacagc  | 1080 |
| tacatacgtg                                | agcttgtaaa  | ctcggttgaaa | tgttatttga  | atgcttagct  | tacataatat  | 1140 |
| tacttaatga                                | gtttct      |             |             |             |             |      |

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..352

(D) OTHER INFORMATION: / Ceres Seq. ID 1597361

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1217:

| SEQUENCE DESCRIPTION: SEQ ID NO:1214 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|--------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val                                  | Arg | Leu | Glu | Glu | Gly | Thr | Val | Lys | Ser | Leu | Ile | Glu | Glu | Lys | Gly |  |
| 1                                    |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Val                                  | Ile | Lys | Gly | Val | Thr | Tyr | Lys | Asn | Lys | Ala | Gly | Glu | Glu | Thr | Thr |  |
|                                      |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |
| Ala                                  | Leu | Ala | Pro | Leu | Thr | Val | Val | Cys | Asp | Gly | Cys | Tyr | Ser | Asn | Leu |  |
|                                      |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |
| Arg                                  | Arg | Ser | Leu | Asn | Asp | Asn | Asn | Ala | Glu | Val | Leu | Ser | Tyr | Gln | Val |  |
|                                      | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |  |
| Ala                                  | Tyr | Ile | Ser | Lys | Asn | Cys | Arg | Leu | Asp | Asp | Pro | Lys | Asn | Leu | His |  |
| 65                                   |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Leu                                  | Ile | Met | Ser | Lys | Pro | Ser | Tyr | Ile | Met | Leu | Tyr | Gln | Leu | Ser | Ser |  |
|                                      |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Thr                                  | Asp | Val | Arg | Cys | Gly | Phe | Glu | Leu | Phe | Ser | Ala | Asn | Phe | Pro | Ser |  |
|                                      |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Ile                                  | Ala | Lys | Gly | Glu | Met | Ala | Thr | Phe | Ala | Lys | Asn | Thr | Leu | Ala | Pro |  |
|                                      |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |
| Gln                                  | Val | Pro | Pro | Lys | Leu | Arg | Lys | Ile | Phe | Leu | Lys | Gly | Leu | Asp | Glu |  |
|                                      | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Gly                                  | Ala | His | Ile | Lys | Ala | Val | Pro | Ala | Lys | Arg | Met | Thr | Ala | Ser | Leu |  |
| 145                                  |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Thr                                  | Lys | Lys | Asn | Gly | Val | Ile | Val | Leu | Gly | Asp | Ala | Phe | Asn | Met | Arg |  |
|                                      |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| His                                  | Xaa | Ser | Val | Ala | Ala | Gly | Met | Met | Val | Leu | Leu | Ser | Asp | Ile | Leu |  |
|                                      |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Ile                                  | Leu | Arg | Arg | Leu | Leu | Gln | Pro | Leu | Ser | Asn | Leu | Gly | Asp | Ala | Asn |  |
|                                      |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |

[illegible]

| SEQUENCE DESCRIPTION: SEQ ID NO: 1 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met                                | Ser | Lys | Pro | Ser | Tyr | Ile | Met | Leu | Tyr | Gln | Leu | Ser | Ser | Thr | Asp |  |
| 1                                  |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Val                                | Arg | Cys | Gly | Phe | Glu | Leu | Phe | Ser | Ala | Asn | Phe | Pro | Ser | Ile | Ala |  |
|                                    |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Lys                                | Gly | Glu | Met | Ala | Thr | Phe | Ala | Lys | Asn | Thr | Leu | Ala | Pro | Gln | Val |  |
|                                    |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Pro                                | Pro | Lys | Leu | Arg | Lys | Ile | Phe | Leu | Lys | Gly | Leu | Asp | Glu | Gly | Ala |  |
|                                    | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| His                                | Ile | Lys | Ala | Val | Pro | Ala | Lys | Arg | Met | Thr | Ala | Ser | Leu | Thr | Lys |  |
| 65                                 |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Lys                                | Asn | Gly | Val | Ile | Val | Leu | Gly | Asp | Ala | Phe | Asn | Met | Arg | His | Xaa |  |
|                                    |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Ser                                | Val | Ala | Ala | Gly | Met | Met | Val | Leu | Leu | Ser | Asp | Ile | Leu | Ile | Leu |  |
|                                    |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Arg                                | Arg | Leu | Leu | Gln | Pro | Leu | Ser | Asn | Leu | Gly | Asp | Ala | Asn | Lys | Val |  |
|                                    |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ser                                | Glu | Val | Ile | Lys | Ser | Phe | Asn | Ile | Ile | Arg | Lys | Pro | Met | Ser | Ala |  |
|                                    | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Thr                                | Val | Asn | Thr | Leu | Gly | Asn | Ala | Phe | Ser | Gln | Val | Leu | Ile | Ala | Ser |  |
| 145                                |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Thr                                | Asp | Glu | Ala | Lys | Glu | Ala | Met | Arg | Gln | Gly | Cys | Tyr | Asp | Tyr | Leu |  |
|                                    |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Ser                                | Ser | Gly | Gly | Phe | Cys | Thr | Ser | Gly | Met | Met | Ala | Leu | Leu | Gly | Gly |  |
|                                    |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Met                                | Asn | Pro | Arg | Pro | Leu | Ser | Leu | Ile | Tyr | His | Leu | Cys | Ala | Ile | Thr |  |
|                                    | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Leu                                | His | Ser | Ile | Gly | His | Leu | Leu | Ser | Pro | Phe | Pro | Ser | Pro | Leu | Ser |  |
|                                    | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Ile                                | Trp | His | Ser | Leu | Arg | Leu | Phe | Gly | Leu | Ala | Leu | Lys | Met | Leu | Val |  |

(2) INFORMATION FOR SEQ ID NO:1219:

(A) LENGTH: 263 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..263

(D) OTHER INFORMATION: / Ceres Seq. ID 1597363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1219:

(2) INFORMATION FOR SEQ ID NO:1220:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 504 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..504

[illegible]

(D) OTHER INFORMATION: / Ceres Seq. ID 1597376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1220:

|            |            |             |             |            |             |     |
|------------|------------|-------------|-------------|------------|-------------|-----|
| aatcacggcg | gcggcgggcg | aagagtagca  | gcagcaggcg  | gcgcgagta  | gcgtctcccc  | 60  |
| acctcgagct | tgccaccatg | gctagaggat  | tgaagaagca  | tttgaagagg | ctcaatgcgc  | 120 |
| ccaagcattg | gatgctggac | aagcttggcg  | gasttttgct  | cccaaaccat | cttctggacc  | 180 |
| tcacaagtct | agggagtgcc | tgccactgat  | cctcatcatc  | aggaacaggc | tcaagtatgc  | 240 |
| tcttacatac | cgtgagtcac | ttccatcctg  | atgcaacgcc  | atgtacttgt | tgatggcaag  | 300 |
| gtcaggacag | acaagacctc | ccctgctggg  | ttcatggatg  | tcatttccat | ccccaaagacc | 360 |
| aacgagaact | acaggctgct | gtatgacact  | aaggggccgct | tccgccttca | cccaatcagg  | 420 |
| gatgaggatg | ctaagttcaa | gcttttgcaag | gttaggtctg  | ttcagtttgg | gcagaagggc  | 480 |
| atcccgtacc | tgaacacgta | tgac        |             |            |             |     |

(2) INFORMATION FOR SEQ ID NO:1221:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1597377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1221:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Arg | Arg | Arg | Arg | Arg | Lys | Ser | Ser | Ser | Ser | Arg | Arg | Arg | Arg | Val |
| 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |
| Ala | Ser | Pro | His | Leu | Glu | Leu | Ala | Thr | Met | Ala | Arg | Gly | Leu | Lys | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Leu | Lys | Arg | Leu | Asn | Ala | Pro | Lys | His | Trp | Met | Leu | Asp | Lys | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Gly | Gly | Xaa | Leu | Leu | Pro | Asn | His | Leu | Leu | Asp | Leu | Thr | Ser | Leu | Gly |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Ala | Cys | His |     |     |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1222:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1597378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1222:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Arg | His | Val | Leu | Val | Asp | Gly | Lys | Val | Arg | Thr | Asp | Lys | Thr |
| 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |
| Tyr | Pro | Ala | Gly | Phe | Met | Asp | Val | Ile | Ser | Ile | Pro | Lys | Thr | Asn | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Tyr | Arg | Leu | Leu | Tyr | Asp | Thr | Lys | Gly | Arg | Phe | Arg | Leu | His | Pro |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ile | Arg | Asp | Glu | Asp | Ala | Lys | Phe | Lys | Leu | Cys | Lys | Val | Arg | Ser | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Phe | Gly | Gln | Lys | Gly | Ile | Pro | Tyr | Leu | Asn | Thr | Tyr | Asp |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1223:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

09668960 "03668960"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1223:

(2) INFORMATION FOR SEQ ID NO:1224:

(ii) MOLECULE TYPE: DNA (genomic)

(D) OTHER INFORMATION: / Ceres Seq. ID 1597392

| (X1) SEQUENCE DESCRIPTION: SEQ ID: 101 |            |            |            |            |            |  |     |
|----------------------------------------|------------|------------|------------|------------|------------|--|-----|
| aatagccttc                             | gcctctcctt | ccagtgctcg | cgcgtgctcg | ctcgctaccc | ctctccctcg |  | 60  |
| aggcctttgc                             | cggcgaagat | cgcccagtcg | cccaccagga | tgaagtttgt | tgctgcctac |  | 120 |
| ctgcttgctg                             | tcctcgtctg | gaactccagc | ccctctgccg | aggacttgac | agccattctg |  | 180 |
| gagtcagttg                             | gctgtgaagt | tgacaatgaa | aagatggaac | tccttctgtc | ccaactgagc |  | 240 |
| ggtaaggaca                             | ttaccgagct | cattgctgct | ggcagggaga | agtttgcttc | agtcccatgt |  | 300 |
| ggcggtgggc                             | ggtgtggctg | ttgtggcagc | tgcccctgct | gctggcgggc | ctctgcgagc |  | 360 |
| tgaggcgaag                             | aaagaagaga | aggtggagga | gaaggaagaa | agtgatgacg | acatgggctt |  | 420 |
| cagcctcttc                             | gactaagcct | gtgcatagtc | aagagtattg | tttttg     |            |  |     |

(2) INFORMATION FOR SEQ ID NO:1225:

(ii) MOLECULE TYPE: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1597393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1225:

| (x1) SEQUENCE DESCRIPTION: 322 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|--------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn 1                          | Ser | Leu | Arg | Leu | Ser | Phe | Gln | Cys | Pro | Pro | Ser | Cys | Ala | Arg | Tyr |
|                                |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro                            | Ser | Pro | Ser | Arg | Pro | Leu | Pro | Ala | Lys | Ser | Ala | Gln | Ser | Pro | Thr |
|                                |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg                            | Met | Lys | Phe | Val | Ala | Ala | Tyr | Leu | Leu | Ala | Val | Leu | Ala | Gly | Asn |
|                                |     |     |     | 35  |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser                            | Ser | Pro | Ser | Ala | Glu | Asp | Leu | Thr | Ala | Ile | Leu | Glu | Ser | Val | Gly |
|                                |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Cys                            | Glu | Val | Asp | Asn | Glu | Lys | Met | Glu | Leu | Leu | Leu | Ser | Gln | Leu | Ser |
| 65                             |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly                            | Lys | Asp | Ile | Thr | Glu | Leu | Ile | Ala | Ala | Gly | Arg | Glu | Lys | Phe | Ala |
|                                |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser                            | Val | Pro | Cys | Gly | Gly | Gly | Arg | Cys | Gly | Cys | Cys | Gly | Ser | Cys | Pro |

100 105 110  
Cys Cys Trp Arg Arg Ser Cys Ser  
115 120  
(2) INFORMATION FOR SEQ ID NO:1226:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 87 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..87  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597394  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1226:  
Met Lys Phe Val Ala Ala Tyr Leu Leu Ala Val Leu Ala Gly Asn Ser  
1 5 10 15  
Ser Pro Ser Ala Glu Asp Leu Thr Ala Ile Leu Glu Ser Val Gly Cys  
20 25 30  
Glu Val Asp Asn Glu Lys Met Glu Leu Leu Leu Ser Gln Leu Ser Gly  
35 40 45  
Lys Asp Ile Thr Glu Leu Ile Ala Ala Gly Arg Glu Lys Phe Ala Ser  
50 55 60  
Val Pro Cys Gly Gly Gly Arg Cys Gly Cys Cys Gly Ser Cys Pro Cys  
65 70 75 80  
Cys Trp Arg Arg Ser Cys Ser  
85

(2) INFORMATION FOR SEQ ID NO:1227:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 502 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..502  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597396  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1227:  
aatagcctcc gcctctcctt ccagtggtccg ccgtcgtgcg ctcgctaccc ctctccctcg 60  
aggcctttgc cgcaagagc gccagtcgc ccaccaggat gaagtttggt gctgcctatc 120  
tgcttgctgt cctcgtggtg aactccagcc cctctgccga ggacttgaca tccattctgg 180  
agtcagttgg ctgtgaagt gacaatgaaa agatggaact ccttctgtcc cagctgagcg 240  
gtaaggacat taccgagctc attgccgccg gcaggagaa gtttgcttca gtcccatgtg 300  
gcggtggcgg tgtggctgtc gcggcastgc ccctgctgct ggcggcgggcg gcgctcctgc 360  
agctgaggcg aagaaagaag agaaggtgga ggagaaggaa gaaagtgatg acgacatggg 420  
cttcagctct tcgactaagt ctgtgcaata gccaaaggga ttgtttttga gtcgaggaag 480  
cagaggggaa gaaaaatagt ag

(2) INFORMATION FOR SEQ ID NO:1228:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 64 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..64  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597397  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1228:  
Ile Ala Ser Ala Ser Pro Ser Ser Val Arg Arg Arg Ala Leu Ala Thr

09689980 "101300

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |  |  |
| Pro | Leu | Pro | Arg | Gly | Leu | Cys | Arg | Glu | Glu | Arg | Pro | Val | Ala | His | Gln |  |  |
|     |     |     | 20  |     |     |     |     |     |     | 25  |     |     |     | 30  |     |  |  |
| Asp | Glu | Val | Cys | Cys | Cys | Leu | Ser | Ala | Cys | Cys | Pro | Arg | Trp | Glu | Leu |  |  |
|     |     | 35  |     |     |     |     |     |     | 40  |     |     | 45  |     |     |     |  |  |
| Gln | Pro | Leu | Cys | Arg | Gly | Leu | Asp | Ile | His | Ser | Gly | Val | Ser | Trp | Leu |  |  |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |  |  |

(2) INFORMATION FOR SEQ ID NO:1229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..123
```

- (D) OTHER INFORMATION: / Ceres Seq. ID 1597398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1229:

Met	Lys	Phe	Val	Ala	Tyr	Leu	Leu	Ala	Val	Leu	Ala	Gly	Asn	Ser	
1			5				10					15			
Ser	Pro	Ser	Ala	Glu	Asp	Leu	Thr	Ser	Ile	Leu	Glu	Ser	Val	Gly	Cys
			20				25						30		
Glu	Val	Asp	Asn	Glu	Lys	Met	Glu	Leu	Leu	Leu	Ser	Gln	Leu	Ser	Gly
			35				40					45			
Lys	Asp	Ile	Thr	Glu	Leu	Ile	Ala	Ala	Gly	Arg	Glu	Lys	Phe	Ala	Ser
	50					55					60				
Val	Pro	Cys	Gly	Gly	Gly	Gly	Val	Ala	Val	Ala	Ala	Xaa	Pro	Leu	Leu
65					70					75					80
Leu	Ala	Ala	Ala	Ala	Leu	Leu	Gln	Leu	Arg	Arg	Arg	Lys	Lys	Arg	Arg
				85					90					95	
Trp	Arg	Arg	Arg	Lys	Lys	Val	Met	Thr	Thr	Trp	Ala	Ser	Ala	Leu	Arg
			100					105					110		
Leu	Ser	Leu	Cys	Asn	Ser	Gln	Gly	Tyr	Cys	Phe					
			115				120								

(2) INFORMATION FOR SEQ ID NO:1230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..85
```

- (D) OTHER INFORMATION: / Ceres Seq. ID 1597399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1230:

[illegible]



(2) INFORMATION FOR SEQ ID NO:1231:

- ```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 509 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
    (A) NAME/KEY: -
    (B) LOCATION: 1..509
    (D) OTHER INFORMATION: / Ceres Seq. ID 1597412
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1231:						
cacccaagtc	caagcaccdn	tcccaaaaaa	atccccatt	ttcttcgagg	cgaggagagc	60
gtgaaagaca	gggcaccgnc	agcgacgatg	tcggggcgcg	gcaagggcgg	caaaggtctg	120
ggcaagggcg	gasaaagcgc	caccgtaagt	ctccgtgaca	acatccaggr	gcatcaccaa	180
gcccgcgatc	cgtagctggc	tcggaggggc	ggcgtgaagc	sattttcggg	gcttatctac	240
gaggagaccc	gcggcgtcct	caagatcttc	ctcgagaacg	tcatecgcga	cgccgtcacc	300
tacaccgagc	acgcacgcgc	caagactggt	accgccatgg	acgtcgtcta	cgcgcctcaag	360
cscagggcgc	aacctctac	ggcttcggag	gctaggctgg	atgcctcttc	tctctgtctgt	420
cgtggatgcg	tgtttgttgt	tagggttact	tcgtttagtt	ccttgtctgt	gacgtgttgg	480
actattgtta	gtagtattct	tgaagttgt				

(2) INFORMATION FOR SEQ ID NO:1232:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 64 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..64
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1597413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1232:																
His	Pro	Ser	Pro	Ser	Thr	Xaa	Pro	Lys	Lys	Ile	Pro	His	Phe	Leu	Arg	
1				5					10					15		
Gly	Glu	Glu	Ser	Val	Lys	Asp	Arg	Ala	Pro	Xaa	Ala	Thr	Met	Ser	Gly	
			20					25					30			
Arg	Gly	Lys	Gly	Gly	Lys	Gly	Leu	Gly	Lys	Gly	Gly	Xaa	Ser	Ala	Thr	
		35					40					45				
Val	Ser	Leu	Arg	Asp	Asn	Ile	Gln	Xaa	His	His	Gln	Ala	Arg	Asp	Pro	
	50					55					60					

(2) INFORMATION FOR SEQ ID NO:1233:

- ```

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 51 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
    (A) NAME/KEY: peptide
    (B) LOCATION: 1..51
    (D) OTHER INFORMATION: / Ceres Seq. ID 1597414

```

| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1233: |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|--------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Pro                                        | Lys | Ser | Lys | His | Xaa | Ser | Gln | Lys | Asn | Pro | Pro | Phe | Ser | Ser | Arg |  |
| 1                                          |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Arg                                        | Gly | Glu | Arg | Glu | Arg | Gln | Gly | Thr | Xaa | Ser | Asp | Asp | Val | Gly | Ala |  |
|                                            |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Arg                                        | Gln | Gly | Arg | Gln | Arg | Ser | Gly | Gln | Gly | Arg | Xaa | Lys | Arg | His | Arg |  |
|                                            |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |

[illegible]

Lys Ser Pro  
50

(2) INFORMATION FOR SEQ ID NO:1234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..57
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597415

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1234:

Met Asp Val Val Tyr Ala Leu Lys Xaa Arg Ala Glu Pro Ser Thr Ala  
1 5 10 15  
Ser Glu Ala Arg Leu Asp Ala Ser Ser Pro Cys Cys Arg Gly Cys Leu  
20 25 30  
Phe Val Val Arg Val Thr Ser Phe Ser Ser Leu Ser Val Thr Cys Trp  
35 40 45  
Thr Ile Val Ser Ser Ile Leu Glu Val  
50 55

(2) INFORMATION FOR SEQ ID NO:1235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..509
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1235:

tngctctcaa atatctctca ccacctctss sctcagcttn tcsscacctt tggtcaggca 60  
ggctcaggca aagggggcgg msaacaagga cgagsgatgg sgaccaaggt catctgcttc 120  
cttgtgctcg catccctgct cctgcgcgtc gcctttcccg tgtctgctct gcgncagcrg 180  
ttogaagaag ggcggcggcg gcggtggtgg cggaggcagt gttagcggaa sgcaggcgcc 240  
aacctgaatc cctgggagtg ctgccccaaag tgcgggctcgc ggtgctccaa gacgcagtac 300  
aggaaggcct gcctcacctt atgcaacaag tgctgcgcca agtgcctctg cgtgccaccg 360  
gggttctacg gcaacaaggg cgctgcccct gctacaacaa ctggaaaacc aaggaaggag 420  
ggcccaagtg cccctagaat aagatccacc gcagctcccg tccgccattg tcscmccttc 480  
tccgaatctg ggaacgtggt gtcatctt

(2) INFORMATION FOR SEQ ID NO:1236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1236:

Xaa Leu Ser Asn Ile Ser His His Leu Xaa Xaa Gln Leu Xaa Xaa Thr  
1 5 10 15  
Phe Gly Gln Ala Gly Ser Gly Lys Gly Gly Xaa Xaa Gln Gly Arg Xaa  
20 25 30  
Met Xaa Thr Lys Val Ile Cys Phe Leu Val Leu Ala Ser Leu Leu Leu  
35 40 45

0963930 "101300

(2) INFORMATION FOR SEQ ID NO:1239:

[illegible]

| (X1) SEQUENCE DESCRIPTION: SEQ ID NO:1059 |            |            |            |            |            |     |
|-------------------------------------------|------------|------------|------------|------------|------------|-----|
| aatttttagga                               | cctaattata | agastctctc | ttagagatgc | tctaaggcac | cgactcgccg | 60  |
| gggacagaga                                | gagagaccga | cgcgccggca | gatcccaagc | tcaccctaga | gggggaagag | 120 |
| ggcgaccgaa                                | gcggcgatgg | gtttcatcat | ggacttcgcg | gagaatctga | tcctccgtct | 180 |
| gatggaggac                                | ccggacaagc | gcgaccaggt | tcggcgggag | catgtctaca | agatgaagga | 240 |
| gcggtgcgag                                | cgcactaagg | cggcgtggag | cctccctctg | cgcccctacg | gcttctggac | 300 |
| cttcgaccgc                                | ttcaactcgc | agctctcctg | ggatccccag | atcagccagg | ccgcggcgct | 360 |
| ncgggacccc                                | tacgacgacc | tcatcgcacg | ccactctggc | tcgcgcgcgt | cttctgaac  | 420 |
| acccgttcgc                                | atctttgccc | agaaggtcta | cttgggcata | aataagaaac | tctttccctt | 480 |
| caaactgatt                                | gt         |            |            |            |            |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Phe | Ile | Met | Asp | Phe | Ala | Glu | Asn | Leu | Ile | Leu | Arg | Leu | Met |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Asp | Pro | Asp | Lys | Arg | Asp | Gln | Val | Arg | Arg | Glu | His | Val | Tyr | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Lys | Glu | Arg | Cys | Glu | Arg | Thr | Lys | Ala | Ala | Trp | Ser | Leu | Pro | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Pro | Tyr | Gly | Phe | Trp | Thr | Phe | Asp | Arg | Phe | Asn | Ser | Gln | Leu | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Trp | Asp | Pro | Gln | Ile | Ser | Gln | Ala | Ala | Gly | Xaa | Arg | Asp | Pro | Tyr | Asp |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Asp | Leu | Ile | Ala | Arg | His | Ser | Gly | Ser | Pro | Pro | Ser | Ser |     |     |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Phe | Ala | Glu | Asn | Leu | Ile | Leu | Arg | Leu | Met | Glu | Asp | Pro | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Arg | Asp | Gln | Val | Arg | Arg | Glu | His | Val | Tyr | Lys | Met | Lys | Glu | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Glu | Arg | Thr | Lys | Ala | Ala | Trp | Ser | Leu | Pro | Leu | Arg | Pro | Tyr | Gly |

[illegible]

35 40 45  
Phe Trp Thr Phe Asp Arg Phe Asn Ser Gln Leu Ser Trp Asp Pro Gln  
50 55 60  
Ile Ser Gln Ala Ala Gly Xaa Arg Asp Pro Tyr Asp Asp Leu Ile Ala  
65 70 75 80  
Arg His Ser Gly Ser Pro Pro Ser Ser  
85

(2) INFORMATION FOR SEQ ID NO:1242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1597429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1242:

Met Glu Asp Pro Asp Lys Arg Asp Gln Val Arg Arg Glu His Val Tyr  
1 5 10 15  
Lys Met Lys Glu Arg Cys Glu Arg Thr Lys Ala Ala Trp Ser Leu Pro  
20 25 30  
Leu Arg Pro Tyr Gly Phe Trp Thr Phe Asp Arg Phe Asn Ser Gln Leu  
35 40 45  
Ser Trp Asp Pro Gln Ile Ser Gln Ala Ala Gly Xaa Arg Asp Pro Tyr  
50 55 60  
Asp Asp Leu Ile Ala Arg His Ser Gly Ser Pro Pro Ser Ser  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 868 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..868

(D) OTHER INFORMATION: / Ceres Seq. ID 1597430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1243:

agaagcttat cgcttatcat ccgcgcctct acatttcttc tctctctgct cctccgcctc 60  
cgctccgcsc tggwtccsat ccaagacagg gatcgccatg tcggactcgg aggagcacca 120  
cttcgaatcg aaggccgacg ctggggcgct caagacctac ccgcagcagg ctggcaccgt 180  
ccgtaagaac ggcttcatcg tcatcaagaa ccgtccctgc aaggttgtgg aggtttctac 240  
ctccaagact ggtaagcatg gccacgcaa atgccacttt gtcgccatag acatattcaa 300  
tgggaaaaaag cttgaagata ttgttccttc atcacacaac tgtgacattc cgcattgtgaa 360  
ccgtactgag tatcagctga ttgatatttc tgaggatgga tttgtgagcc ttcttacttc 420  
agatggcaac actaaggatg atcttagact cccaactgat gagactcttg tggcccagat 480  
taaggaaggg ttcgaaagcg ggaaggatct tgttgtgact gtccagtctg cgatggggga 540  
ggagcagatc tgcgcgctga aggatgttgg ccccaagtaa cttccttggc tttggagacg 600  
gaacctact ctatctcaac ttaaatacgga aaagaagtgt atcaccaaaa ggattgctac 660  
cgagacattc acctggcttg agctbgcttt tgctatagcg tgcaaggggt tgctgggtgt 720  
cgtacctacc tgacttatca ttatctgttg ttacattctg gacctgtat tttctatgct 780  
ttcatgtctc tctactttct agtattaatt atcaataagt tggtttgga tggttgaatt 840  
gcatccaatg catgaagttt ctttggt

(2) INFORMATION FOR SEQ ID NO:1244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..192  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1597431  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1244:

Glu Ala Tyr Arg Leu Ser Ser Ala Pro Leu His Phe Phe Ser Leu Cys  
1                    5                    10                    15  
Ser Ser Ala Ser Ala Ser Xaa Trp Xaa Xaa Ser Lys Thr Gly Ile Ala  
                    20                    25                    30  
Met Ser Asp Ser Glu Glu His His Phe Glu Ser Lys Ala Asp Ala Gly  
                    35                    40                    45  
Ala Ser Lys Thr Tyr Pro Gln Gln Ala Gly Thr Val Arg Lys Asn Gly  
                    50                    55                    60  
Phe Ile Val Ile Lys Asn Arg Pro Cys Lys Val Val Glu Val Ser Thr  
65                    70                    75                    80  
Ser Lys Thr Gly Lys His Gly His Ala Lys Cys His Phe Val Ala Ile  
                    85                    90                    95  
Asp Ile Phe Asn Gly Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His  
                    100                    105                    110  
Asn Cys Asp Ile Pro His Val Asn Arg Thr Glu Tyr Gln Leu Ile Asp  
                    115                    120                    125  
Ile Ser Glu Asp Gly Phe Val Ser Leu Leu Thr Ser Asp Gly Asn Thr  
130                    135                    140  
Lys Asp Asp Leu Arg Leu Pro Thr Asp Glu Thr Leu Val Ala Gln Ile  
145                    150                    155                    160  
Lys Glu Gly Phe Glu Ser Gly Lys Asp Leu Val Val Thr Val Gln Ser  
                    165                    170                    175  
Ala Met Gly Glu Glu Ile Cys Ala Leu Lys Asp Val Gly Pro Lys  
                    180                    185                    190

(2) INFORMATION FOR SEQ ID NO:1245:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 160 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..160  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1597432  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1245:

Met Ser Asp Ser Glu His His Phe Glu Ser Lys Ala Asp Ala Gly  
1                    5                    10                    15  
Ala Ser Lys Thr Tyr Pro Gln Gln Ala Gly Thr Val Arg Lys Asn Gly  
                    20                    25                    30  
Phe Ile Val Ile Lys Asn Arg Pro Cys Lys Val Val Glu Val Ser Thr  
                    35                    40                    45  
Ser Lys Thr Gly Lys His Gly His Ala Lys Cys His Phe Val Ala Ile  
                    50                    55                    60  
Asp Ile Phe Asn Gly Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His  
65                    70                    75                    80  
Asn Cys Asp Ile Pro His Val Asn Arg Thr Glu Tyr Gln Leu Ile Asp  
                    85                    90                    95  
Ile Ser Glu Asp Gly Phe Val Ser Leu Leu Thr Ser Asp Gly Asn Thr  
                    100                    105                    110  
Lys Asp Asp Leu Arg Leu Pro Thr Asp Glu Thr Leu Val Ala Gln Ile  
                    115                    120                    125

09639980-101300

Lys Glu Gly Phe Glu Ser Gly Lys Asp Leu Val Val Thr Val Gln Ser  
130 135 140  
Ala Met Gly Glu Glu Gln Ile Cys Ala Leu Lys Asp Val Gly Pro Lys  
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:1246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..239
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1246:

acagcatctc aagtcttcac actcctcgcc atcacataaa accagtgcaa gcagaagcag 60  
cgcaatggcg agcagcacca tggccctctc ctccacagcc ttccgcccga akgcagtga 120  
cgtgccgtcg tctctcwtcg gcgangcccgc cgtgacgatg cgcaagangg cggcgaakgc 180  
aaagccggcg gcgagctccg gcagcccggtg gtacggcccc gamcgcgtgc tctacctgg

(2) INFORMATION FOR SEQ ID NO:1247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1247:

Gln His Leu Lys Ser Ser His Ser Ser Pro Ser His Lys Thr Ser Ala  
1 5 10 15  
Ser Arg Ser Ser Ala Met Ala Ser Ser Thr Met Ala Leu Ser Ser Thr  
20 25 30  
Ala Phe Ala Gly Xaa Ala Val Asn Val Pro Ser Ser Leu Xaa Gly Xaa  
35 40 45  
Ala Arg Val Thr Met Arg Lys Xaa Ala Ala Xaa Ala Lys Pro Ala Ala  
50 55 60  
Ser Ser Gly Ser Pro Trp Tyr Gly Pro Xaa Arg Val Leu Tyr Leu  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..58
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1248:

Met Ala Ser Ser Thr Met Ala Leu Ser Ser Thr Ala Phe Ala Gly Xaa  
1 5 10 15  
Ala Val Asn Val Pro Ser Ser Leu Xaa Gly Xaa Ala Arg Val Thr Met  
20 25 30  
Arg Lys Xaa Ala Ala Xaa Ala Lys Pro Ala Ala Ser Ser Gly Ser Pro

09689980-101300

45

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..53

- (D) OTHER INFORMATION: / Ceres Seq. ID 1597440

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1249:

(2) INFORMATION FOR SEQ ID NO:1250:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..130

- (D) OTHER INFORMATION: / Ceres Seq. ID 1597452

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1250:

tctcccaaag ccatcttctt ccgcgggact agttttttct gaagattcgg cgatggcggc 60  
gacgatccaa tccgtgaagg cgcgccagat ctttgacagc cgcggcaacc ctacagtcga 120  
ggtcgcagtg

(2) INFORMATION FOR SEQ ID NO:1251:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..43

- (D) OTHER INFORMATION: / Ceres Seq. ID 1597453

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1251:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Pro | Lys | Pro | Ser | Ser | Phe | Arg | Gly | Leu | Val | Phe | Ser | Glu | Asp | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Met | Ala | Ala | Thr | Ile | Gln | Ser | Val | Lys | Ala | Arg | Gln | Ile | Phe | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Arg | Gly | Asn | Pro | Thr | Val | Glu | Val | Asp | Val |     |     |     |     |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1252:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 base pairs

- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single



- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..446  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1597456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1252:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| aagctcctcg | tcaccagtca  | gaaaacagtg | ggatcgagtt | gtttcactgc | acgagcacat | 60  |
| cctccggcga | ccaccggcct  | ccctctccgt | cctctagcga | ccgaccaacg | cgtcgagcga | 120 |
| agatgtcgtg | gcagacgtac  | gtggacgagc | aaccctggat | gtgcgagatc | gagggccacc | 180 |
| acctcacgtc | ggcgcccatc  | gtcggccacg | rgcgccacct | gggtcagag  | caccgcattc | 240 |
| cccagattca | agcccagagga | gatggctgcc | atcatgaagg | atttcgacga | gccggggcac | 300 |
| tcgccccgac | cggcctgata  | ctgggaggca | ccaagtacat | ggtcattcaa | gtcgaacctg | 360 |
| gagctgtcat | ccgtggcaag  | aagggatccg | ggggcatcac | tgtgaagaaa | acagggcagt | 420 |
| cactcatcat | tggcatctac  | gacgag     |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1253:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 105 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..105  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1597457

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1253:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Leu | Leu | Val | Thr | Ser | Gln | Lys | Thr | Val | Gly | Ser | Ser | Cys | Phe | Thr |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Arg | Ala | His | Pro | Pro | Ala | Thr | Thr | Gly | Leu | Pro | Leu | Arg | Pro | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Thr | Asp | Gln | Arg | Val | Glu | Arg | Arg | Cys | Arg | Gly | Arg | Arg | Thr | Trp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Ser | Asn | Pro | Gly | Cys | Ala | Arg | Ser | Arg | Ala | Thr | Thr | Ser | Arg | Arg |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Arg | Pro | Ser | Ser | Ala | Thr | Xaa | Ala | Thr | Trp | Ala | Gln | Ser | Thr | Ala | Phe |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Glu | Phe | Lys | Pro | Glu | Glu | Met | Ala | Ala | Ile | Met | Lys | Asp | Phe | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Glu | Pro | Gly | His | Ser | Pro | Arg | Pro | Ala |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1254:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 148 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..148  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1597458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1254:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Pro | Arg | His | Gln | Ser | Glu | Asn | Ser | Gly | Ile | Glu | Leu | Phe | His | Cys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Ser | Thr | Ser | Ser | Gly | Asp | His | Arg | Pro | Pro | Ser | Pro | Ser | Ser | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Arg | Pro | Thr | Arg | Arg | Ala | Lys | Met | Ser | Trp | Gln | Thr | Tyr | Val | Asp |
|     |     |     | 35  |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Glu | Gln | Pro | Trp | Met | Cys | Glu | Ile | Glu | Gly | His | His | Leu | Thr | Ser | Ala |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

Ala Ile Val Gly His Xaa Arg His Leu Gly Ser Glu His Arg Ile Pro  
65 70 75 80  
Arg Val Gln Ala Arg Gly Asp Gly Cys His His Glu Gly Phe Arg Arg  
85 90 95  
Ala Gly Ala Leu Ala Pro Thr Gly Leu Ile Leu Gly Gly Thr Lys Tyr  
100 105 110  
Met Val Ile Gln Val Glu Pro Gly Ala Val Ile Arg Gly Lys Lys Gly  
115 120 125  
Ser Gly Gly Ile Thr Val Lys Lys Thr Gly Gln Ser Leu Ile Ile Gly  
130 135 140  
Ile Tyr Asp Glu  
145

(2) INFORMATION FOR SEQ ID NO:1255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1255:

Met Ser Trp Gln Thr Tyr Val Asp Glu Gln Pro Trp Met Cys Glu Ile  
1 5 10 15  
Glu Gly His His Leu Thr Ser Ala Ala Ile Val Gly His Xaa Arg His  
20 25 30  
Leu Gly Ser Glu His Arg Ile Pro Arg Val Gln Ala Arg Gly Asp Gly  
35 40 45  
Cys His His Glu Gly Phe Arg Arg Ala Gly Ala Leu Ala Pro Thr Gly  
50 55 60  
Leu Ile Leu Gly Gly Thr Lys Tyr Met Val Ile Gln Val Glu Pro Gly  
65 70 75 80  
Ala Val Ile Arg Gly Lys Lys Gly Ser Gly Gly Ile Thr Val Lys Lys  
85 90 95  
Thr Gly Gln Ser Leu Ile Ile Gly Ile Tyr Asp Glu  
100 105

(2) INFORMATION FOR SEQ ID NO:1256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..472
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1256:

atctcagcag tgacgaactc gaagcttgck ttcttgtagt agaggtcggc agcaagcggg 60  
ggtagagcga gaggtcgaga agatgaagag cagcactctg ttggcgatcc tagttctcca 120  
ggcccttctg gtctctgcgg ccgtggcaaa ggacctgcag ggccgacgac gaagaagcag 180  
tgctggttgc ggcgagtgc ccasctggtc gggcgtgtgg acctgcgacg acctcctcac 240  
caagtgcgcc gccacctgca agaactgcgt ccccggtgtc acggacaagg gggccatcaa 300  
gtacaggtgc cgcgacttcc tccccgaaaa ctgcggctgc aagatccact agagactcat 360  
ccaattccac catggccgcg cgccacagcg gcacagccga ttggatcctt ccatgttctt 420  
ccgtccgtcc gccttgctac aagcaggcag ccacaccaat aagctagctc tt

(2) INFORMATION FOR SEQ ID NO:1257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids

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- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..89  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597477  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1257:

Met Lys Ser Ser Thr Leu Leu Ala Ile Leu Val Leu Gln Ala Leu Leu  
1 5 10 15  
Val Ser Ala Ala Val Ala Lys Asp Leu Gln Gly Arg Arg Arg Arg Ser  
20 25 30  
Ser Ala Gly Cys Gly Glu Cys Thr Xaa Trp Ser Gly Val Trp Thr Cys  
35 40 45  
Asp Asp Leu Leu Thr Lys Cys Ala Ala Thr Cys Lys Asn Cys Val Pro  
50 55 60  
Val Ser Thr Asp Lys Gly Ala Ile Lys Tyr Arg Cys Arg Asp Phe Leu  
65 70 75 80  
Pro Glu Asn Cys Gly Cys Lys Ile His  
85

(2) INFORMATION FOR SEQ ID NO:1258:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 406 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..406  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597478  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1258:

accaaggaaa ttcacaaagc gcctagcaaa agcatacttc ccgaagcact cttgcaatcc 60  
actgagttct gtttgttgag acgcatagag ctagctgcta gcgtcgacaa tgctcgctcgt 120  
gaggcgacag aacgtgttcg accccttctc gatggacctc tgggatccct tcgacaccat 180  
gttcgcgtcc atcgtcccgt cggcgacctc caccaactcc gagactgccg ccttcgccag 240  
cgcccgcatc gactggaagg agacgcccga ggsgcacgtc ttcaaggccg acctccccgg 300  
cgtcaagaag gaggaggtca aggtcgaggt cgaagmggnc aacgtgctgg tcatcagcgg 360  
ccagcgcasa gggagaagga ggacaaggac gacaagtggc accgcg

(2) INFORMATION FOR SEQ ID NO:1259:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 135 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..135  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597479  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1259:

Thr Lys Glu Ile His Lys Ala Pro Ser Lys Ser Ile Leu Pro Glu Ala  
1 5 10 15  
Leu Leu Gln Ser Thr Glu Phe Cys Leu Leu Arg Arg Ile Glu Leu Ala  
20 25 30  
Ala Ser Val Asp Asn Val Ala Arg Glu Ala His Glu Arg Val Arg Pro  
35 40 45  
Leu Leu Asp Gly Pro Leu Gly Ser Leu Arg His His Val Pro Leu His  
50 55 60  
Arg Pro Val Gly Asp Leu His Gln Leu Arg Asp Cys Arg Leu Arg Gln

09589980-101300

65 70 75 80  
Arg Pro His Arg Leu Glu Gly Asp Ala Arg Xaa Ala Arg Leu Gln Gly  
85 90 95  
Arg Pro Pro Arg Arg Gln Glu Gly Gly Gly Gln Gly Arg Gly Arg Xaa  
100 105 110  
Xaa Gln Arg Ala Gly His Gln Arg Pro Ala Xaa Arg Glu Lys Glu Asp  
115 120 125  
Lys Asp Asp Lys Trp His Arg  
130 135

(2) INFORMATION FOR SEQ ID NO:1260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1597480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1260:

Met Ser Leu Val Arg Arg Thr Asn Val Phe Asp Pro Phe Ser Met Asp  
1 5 10 15  
Leu Trp Asp Pro Phe Asp Thr Met Phe Arg Ser Ile Val Pro Ser Ala  
20 25 30  
Thr Ser Thr Asn Ser Glu Thr Ala Ala Phe Ala Ser Ala Arg Ile Asp  
35 40 45  
Trp Lys Glu Thr Pro Glu Xaa His Val Phe Lys Ala Asp Leu Pro Gly  
50 55 60  
Val Lys Lys Glu Glu Val Lys Val Glu Val Glu Xaa Xaa Asn Val Leu  
65 70 75 80  
Val Ile Ser Gly Gln Arg Xaa Gly Arg Arg Arg Thr Arg Thr Thr Ser  
85 90 95  
Gly Thr Ala

(2) INFORMATION FOR SEQ ID NO:1261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1597481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1261:

Met Asp Leu Trp Asp Pro Phe Asp Thr Met Phe Arg Ser Ile Val Pro  
1 5 10 15  
Ser Ala Thr Ser Thr Asn Ser Glu Thr Ala Ala Phe Ala Ser Ala Arg  
20 25 30  
Ile Asp Trp Lys Glu Thr Pro Glu Xaa His Val Phe Lys Ala Asp Leu  
35 40 45  
Pro Gly Val Lys Lys Glu Glu Val Lys Val Glu Val Glu Xaa Xaa Asn  
50 55 60  
Val Leu Val Ile Ser Gly Gln Arg Xaa Gly Arg Arg Arg Thr Arg Thr  
65 70 75 80  
Thr Ser Gly Thr Ala  
85

(2) INFORMATION FOR SEQ ID NO:1262:

(i) SEQUENCE CHARACTERISTICS:

09688880-101300

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..463
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1262:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| accacagcat ccgcrtttcc ccgaccacac cgttcctccg agcccaggag cacccccgcg  | 60  |
| ccaggaggaa gtttgtttctt ttaacaatat gtcgagggag gagaatgttt acatggccaa | 120 |
| gttggctgag caggctgaaa ggtatgagga gatggttgag tatatggaga aggtggctaa  | 180 |
| gactgtagat gtggaagagc tctactgttg ggagcgtaac cttctgtctg ttgcatacaa  | 240 |
| gaatgtgatt ggggctcgcc gcgcttcatt gcgcattgtt tcttccattg aacaaaagga  | 300 |
| ggagtcccgt aagaacgaag agcatgtgaa ccttatcaag gaatatcgtg gcaagatcga  | 360 |
| ggctgaactg agcaatatct gtgatggaat cttgaagctg cttgactccc acctagtgc   | 420 |
| ttcttctact gctgctgaat caaaggtctt ctacctcaag atg                    |     |

(2) INFORMATION FOR SEQ ID NO:1263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1263:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Gln | His | Pro | Xaa | Phe | Pro | Asp | His | Thr | Val | Pro | Pro | Ser | Pro | Gly |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Pro | Pro | Arg | Gln | Glu | Glu | Val | Cys | Ser | Phe | Asn | Asn | Met | Ser | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Glu | Asn | Val | Tyr | Met | Ala | Lys | Leu | Ala | Glu | Gln | Ala | Glu | Arg | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Glu | Met | Val | Glu | Tyr | Met | Glu | Lys | Val | Ala | Lys | Thr | Val | Asp | Val |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Glu | Leu | Thr | Val | Glu | Glu | Arg | Asn | Leu | Leu | Ser | Val | Ala | Tyr | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asn | Val | Ile | Gly | Ala | Arg | Arg | Ala | Ser | Trp | Arg | Ile | Val | Ser | Ser | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Glu | Gln | Lys | Glu | Glu | Ser | Arg | Lys | Asn | Glu | Glu | His | Val | Asn | Leu | Ile |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Glu | Tyr | Arg | Gly | Lys | Ile | Glu | Ala | Glu | Leu | Ser | Asn | Ile | Cys | Asp |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Gly | Ile | Leu | Lys | Leu | Leu | Asp | Ser | His | Leu | Val | Pro | Ser | Ser | Thr | Ala |
| 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Ala | Glu | Ser | Lys | Val | Phe | Tyr | Leu | Lys | Met |     |     |     |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597484

09669960 "101300"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1264:  
Met Ser Arg Glu Glu Asn Val Tyr Met Ala Lys Leu Ala Glu Gln Ala  
1 5 10 15  
Glu Arg Tyr Glu Glu Met Val Glu Tyr Met Glu Lys Val Ala Lys Thr  
20 25 30  
Val Asp Val Glu Glu Leu Thr Val Glu Glu Arg Asn Leu Leu Ser Val  
35 40 45  
Ala Tyr Lys Asn Val Ile Gly Ala Arg Arg Ala Ser Trp Arg Ile Val  
50 55 60  
Ser Ser Ile Glu Gln Lys Glu Glu Ser Arg Lys Asn Glu Glu His Val  
65 70 75 80  
Asn Leu Ile Lys Glu Tyr Arg Gly Lys Ile Glu Ala Glu Leu Ser Asn  
85 90 95  
Ile Cys Asp Gly Ile Leu Lys Leu Leu Asp Ser His Leu Val Pro Ser  
100 105 110  
Ser Thr Ala Ala Glu Ser Lys Val Phe Tyr Leu Lys Met  
115 120 125

(2) INFORMATION FOR SEQ ID NO:1265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1265:

Met Ala Lys Leu Ala Glu Gln Ala Glu Arg Tyr Glu Met Val Glu  
1 5 10 15  
Tyr Met Glu Lys Val Ala Lys Thr Val Asp Val Glu Glu Leu Thr Val  
20 25 30  
Glu Glu Arg Asn Leu Leu Ser Val Ala Tyr Lys Asn Val Ile Gly Ala  
35 40 45  
Arg Arg Ala Ser Trp Arg Ile Val Ser Ser Ile Glu Gln Lys Glu Glu  
50 55 60  
Ser Arg Lys Asn Glu Glu His Val Asn Leu Ile Lys Glu Tyr Arg Gly  
65 70 75 80  
Lys Ile Glu Ala Glu Leu Ser Asn Ile Cys Asp Gly Ile Leu Lys Leu  
85 90 95  
Leu Asp Ser His Leu Val Pro Ser Ser Thr Ala Ala Glu Ser Lys Val  
100 105 110  
Phe Tyr Leu Lys Met  
115

(2) INFORMATION FOR SEQ ID NO:1266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..401
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597499

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1266:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| agaaacccta acactcatca cgccgccact gatctgctct gttgctggtg actaggagca | 60  |
| gtagcgrnga gggattcttg atggccaagt cgaagaacca cacggcgcat aaccagtcgt | 120 |
| tcaaggcgca caagaacggc atcaagaagc ccaagcgcca ccgccagacc tccaccaagg | 180 |
| ggatggaccc gaagtttctg aggaacttga ggtactcaar gaagggcaac aagaagagt  | 240 |

0969980 "101000

(2) INFORMATION FOR SEQ ID NO:1267:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..60

(D) OTHER INFORMATION: / Ceres Seq. ID 1597500

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1267:

Met Ala Lys Ser Lys Asn His Thr Ala His Asn Gln Ser Phe Lys Ala  
1 5 10 15

His Lys Asn Gly Ile Lys Lys Pro Lys Arg His Arg Gln Thr Ser Thr

Lys Gly Met Asp Pro Lys Phe Leu Arg Asn Leu Arg Tyr Ser Xaa Lys

Gly Asn Lys Lys Ser Gly Glu Ala Glu Ser Glu Glu  
50 55 60

(2) INFORMATION FOR SEQ ID NO:1268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 456 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..456

(D) OTHER INFORMATION: / Ceres Seq. ID 1597502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1268:

|             |            |             |            |            |            |     |
|-------------|------------|-------------|------------|------------|------------|-----|
| aaactacacc  | acaccgcacc | ggcaccacca  | ccaaccgagc | ggnnccaggc | tctgtctcag | 60  |
| gaagggggaga | agaggcgagc | cttccttggg  | aagtcgcagg | aggagagaag | gggaacaaag | 120 |
| atgggggcgcg | gcaagatcga | gatcaagcgg  | atcgagaact | ccaccaaccg | ccagtgcact | 180 |
| tctccaagcg  | ccgcaacggg | atcctcaaga  | aggcgcggga | gatcagcgtg | ctctgcgcag | 240 |
| ccgaggtcgg  | cgtctcgtct | tctccagcgc  | cggcaaagtg | taccgggggt | cattggtcga | 300 |
| gtgcgaggat  | aactggaatt | gccagctcga  | gaacataacc | ttaactgcc  | aggatgggaa | 360 |
| ggtttcgcag  | tctggagcag | tcttcattcag | aggaagcaga | gtbagattta | tgattatacc | 420 |
| tqatatgtct  | aagaacgctc | ccatgttcaa  | gcgcctt    |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1269:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1597503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1269:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Tyr | Thr | Thr | Pro | His | Arg | His | His | His | Gln | Pro | Ser | Xaa | Xaa | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Leu Leu Leu Arg Lys Gly Arg Arg Gly Glu Pro Ser Leu Gly Ser Arg  
20 25 30

Arg Arg Arg Glu Gly Glu Gln Arg Trp Gly Ala Ala Arg Ser Arg Ser  
35 40 45

[illegible]

Ser Gly Ser Arg Thr Pro Pro Thr Ala Ser Asp Leu Leu Gln Ala Pro  
50 55 60  
Gln Arg Asp Pro Gln Glu Gly Ala Gly Asp Gln Arg Ala Leu Arg Arg  
65 70 75 80  
Arg Gly Arg Arg Leu Val Phe Ser Ser Ala Gly Lys Val Tyr Arg Gly  
85 90 95  
Ser Leu Val Glu Cys Glu Asp Asn Trp Asn Cys Gln Leu Glu Asn Ile  
100 105 110  
Thr Phe Thr Ala Lys Asp Gly Lys Val Ser Gln Leu Glu His Val Phe  
115 120 125  
Ile Arg Gly Ser Arg Xaa Arg Phe Met Ile Ile Pro Asp Met Leu Lys  
130 135 140  
Asn Ala Pro Met Phe Lys Arg  
145 150

(2) INFORMATION FOR SEQ ID NO:1270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1270:

Thr Thr Pro His Arg Thr Gly Thr Thr Thr Asn Arg Ala Xaa Pro Gly  
1 5 10 15  
Ser Cys Ser Gly Arg Gly Glu Glu Ala Ser Leu Pro Trp Glu Val Ala  
20 25 30  
Gly Gly Glu Lys Gly Asn Lys Asp Gly Ala Arg Gln Asp Arg Asp Gln  
35 40 45  
Ala Asp Arg Glu Leu His Gln Pro Pro Val Thr Phe Ser Lys Arg Arg  
50 55 60  
Asn Gly Ile Leu Lys Lys Ala Arg Glu Ile Ser Val Leu Cys Asp Ala  
65 70 75 80  
Glu Val Gly Val Ser Ser Ser Pro Ala Pro Ala Lys Cys Thr Gly Gly  
85 90 95  
His Trp Ser Ser Ala Arg Ile Thr Gly Ile Ala Ser Ser Arg Thr  
100 105 110

(2) INFORMATION FOR SEQ ID NO:1271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..494
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1271:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| atcaactcgc aattccgcac tcgttccaac tcctgagcac tttctcctcg tcccagacaa   | 60  |
| gccaatcgaa gccgagatac gaccatggac tccaccggca ccggagcagg gggtaggggg   | 120 |
| aagaagggag cggccgggag caaggtcggc gggccaagga agaagtcggt gtcgaggtcc   | 180 |
| gtgaaggccg gtctccagtt ccccgctcggc cgcacgaggc gctacttgaa gaagggccgc  | 240 |
| tacgcgcang ttcggcacccg gcgcccccgct ctacctcgcc gctgtcctcg aatacctcgc | 300 |
| cgcgtgaggtt ctggagctcg ccggtaatgc tgccaggagc aaggcgatca agaggtttca  | 360 |
| ggtkaggaac atcgtggaac aggcggccat caggacgctc caggaagcat gcgtctatga   | 420 |
| tggctacgtc ctcccgaagc tgtacgcaa ggtgcaccac tgcgtctcgt gcgcgatcca    | 480 |
| mgstcacatc gtcc                                                     |     |



(i) SEQUENCE CHARACTERISTICS:

- |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Thr | Arg | Asn | Ser | Ala | Phe | Val | Pro | Thr | Pro | Glu | His | Phe | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Pro | Asp | Lys | Pro | Ile | Glu | Ala | Glu | Ile | Arg | Pro | Trp | Thr | Pro | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Pro | Glu | Gln | Gly | Val | Arg | Gly | Arg | Arg | Glu | Arg | Pro | Gly | Ala | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Ala | Gly | Gln | Gly | Arg | Ser | Arg | Cys | Arg | Gly | Pro |     |     |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

- [illegible]

(i) SEQUENCE CHARACTERISTICS:

- |                                            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|--------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1274: |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Met                                        | Leu | Pro | Gly | Thr | Arg | Arg | Ser | Arg | Gly | Phe | Arg | Xaa | Gly | Thr | Ser |
| 1                                          |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Trp                                        | Asn | Arg | Arg | Pro | Ser | Gly | Thr | Ser | Arg | Lys | His | Ala | Ser | Met | Met |
|                                            |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala                                        | Thr | Ser | Ser | Arg | Ser | Cys | Thr | Pro | Arg | Cys | Thr | Thr | Ala | Ser | Arg |
|                                            |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala                                        | Arg | Ser | Xaa | Xaa | Thr | Ser | Ser |     |     |     |     |     |     |     |     |

55

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1275:

(2) INFORMATION FOR SEQ ID NO:1276:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1276:

(2) INFORMATION FOR SEQ ID NO:1277:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1277:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Ser | Thr | Gly | Thr | Gly | Ala | Gly | Gly | Lys | Gly | Lys | Xaa | Gly | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Gly | Arg | Lys | Val | Gly | Gly | Pro | Arg | Lys | Lys | Ser | Val | Ser | Arg | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Lys | Ala | Gly | Leu | Gln | Phe | Pro | Val | Gly | Arg | Ile | Gly | Arg | Tyr | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Lys | Gly | Arg | Tyr | Ala | Xaa | Cys | Xaa | Ala | Pro | Ala | Pro | Pro | Ser | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ser | Xaa | Leu | Ser | Ser | Asn | Thr | Xaa | Pro | Xaa | Phe | Leu | Xaa | Thr | Xaa | Xaa |

(2) INFORMATION FOR SEQ ID NO:1278:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1278:

(2) INFORMATION FOR SEQ ID NO:1279:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1279:

(2) INFORMATION FOR SEQ ID NO:1280:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1280:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Ser | Ala | Arg | Leu | Gln | Gln | Gly | Arg | Pro | Val | Ala | Phe | Leu | Leu | Arg |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gly | Pro | Trp | Ala | Val | Leu | Pro | Ala | Val | Ala | Ser | Ser | Pro | Arg | Leu | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

Gly Arg Thr Gln Asp Cys Asn Arg Val Val Arg Arg His Gln Leu Leu  
35 40 45  
Ala Gln Ser  
50

(2) INFORMATION FOR SEQ ID NO:1281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..94  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1281:

| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met                                     | Ala | Ser | Phe |     | Ser | Glu | Ala | Pro | Pro | Gly | Asn | Pro | Thr | Ala | Gly | Glu |
| 1                                       |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys                                     | Ile | Phe | Lys | Thr | Lys | Cys | Ala | Gln | Cys | His | Thr | Val | Asp | Lys | Gly |     |
|                                         |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ala                                     | Gly | His | Lys | Gln | Gly | Pro | Asn | Leu | Asn | Gly | Leu | Phe | Gly | Arg | Gln |     |
|                                         |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ser                                     | Gly | Thr | Thr | Pro | Gly | Tyr | Ser | Tyr | Ser | Ser | Ala | Asn | Lys | Asn | Met |     |
|                                         | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Ala                                     | Val | Ile | Trp | Glu | Glu | Asn | Thr | Leu | Tyr | Asp | Tyr | Leu | Leu | Asn | Pro |     |
| 65                                      |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys                                     | Lys | Tyr | Ile | Pro | Gly | Thr | Lys | Met | Val | Phe | Pro | Gly | Leu |     |     |     |
|                                         |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..116  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1282:

(X1) SEQUENCE DESCRIPTION: SEQ ID: NO:101

cnaaaaaagg tacatcatcat ctcttccaaa tcccaccagc aaatccccaa ttcctccgag 60  
ttcgagcgcac catgtcgggg cgtggcaagg gcgggaaggg tctgggcaaa ggcggc

(2) INFORMATION FOR SEQ ID NO:1283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..38  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1283:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1284:

```

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 38 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
    (A) NAME/KEY: peptide
    (B) LOCATION: 1..38
    (D) OTHER INFORMATION: / Ceres Seq. ID 1597581
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1284:
Xaa Lys Arg Tyr Thr Ser Ser Leu Pro Asn Pro Thr Ser Lys Ser Pro
1          5          10          15
Ile Pro Pro Ser Ser Asp His Val Gly Ala Trp Gln Gly Arg Glu
          20          25          30
Gly Ser Gly Gln Arg Arg
          35

```

```
(2) INFORMATION FOR SEQ ID NO:1285:
```

```
      (i) SEQUENCE CHARACTERISTICS:  
            (A) LENGTH: 38 amino acids  
            (B) TYPE: amino acid  
            (C) STRANDEDNESS:  
            (D) TOPOLOGY: linear  
      (ii) MOLECULE TYPE: peptide  
      (ix) FEATURE:  
            (A) NAME/KEY: peptide  
            (B) LOCATION: 1..38  
            (D) OTHER INFORMATION: / Ceres Seq. ID 1597582  
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1285:
```

```
Lys Lys Gly Thr His His Leu Phe Gln Ile Pro Pro Ala Asn Pro Gln  
1                                     10                      15  
Phe Leu Arg Val Arg Ala Thr Met Ser Gly Arg Gly Lys Gly Gly Lys  
                20                        25                    30  
Gly Leu Gly Lys Gly Gly
```

```
          35
```

```
(2) INFORMATION FOR SEQ ID NO:1286:
  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 486 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear
  (ii) MOLECULE TYPE: DNA (genomic)
  (ix) FEATURE:
      (A) NAME/KEY: -
      (B) LOCATION: 1..486
      (D) OTHER INFORMATION: / Ceres Seq. ID 1597589
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1286:
accgcagcca caccccaaca tcaaaaccct cccatctctt cccctccgcc gccgtctctg      60
ctctcaagat cgccatggcg tcagaaaaga agcagtcgaa cccgatgcgg gagatcaagg      120
tgcagaagct cgtgctcaat atctccgttg gagagagtgg agatcgactc acccgcgccg      180
ccaaggtggt ggagcagttg agtgggcagt ctccggtttt ctccaaggca aggtatactg      240
tgagggtctt cggtattcgt cgtaatgaga agattgcatg ctacgttacg gtcaggggtg      300
agaaggcaat gcagcttctt gagagtggcc tcaaggtgaa ggagtatgag cttctgagga      360
ggaacttcag tgatactggc tgctttggtt ttggtattca ggagcacatt gatcttgaa      420
tcaagtatga cccgtctact ggtatttatn gcatggactt ttacgtcggt ctggaacgag      480
ctcatt
```

(2) INFORMATION FOR SEQ ID NO:1287:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 161 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..161  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597590

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1287:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | His | Thr | Pro | Thr | Ser | Lys | Pro | Ser | His | Leu | Phe | Pro | Ser | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ala | Val | Ser | Ala | Leu | Lys | Ile | Ala | Met | Ala | Ser | Glu | Lys | Lys | Gln | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Pro | Met | Arg | Glu | Ile | Lys | Val | Gln | Lys | Leu | Val | Leu | Asn | Ile | Ser |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Val | Gly | Glu | Ser | Gly | Asp | Arg | Leu | Thr | Arg | Ala | Ala | Lys | Val | Leu | Glu |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Gln | Leu | Ser | Gly | Gln | Ser | Pro | Val | Phe | Ser | Lys | Ala | Arg | Tyr | Thr | Val |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Ser | Phe | Gly | Ile | Arg | Arg | Asn | Glu | Lys | Ile | Ala | Cys | Tyr | Val | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Val | Arg | Gly | Glu | Lys | Ala | Met | Gln | Leu | Leu | Glu | Ser | Gly | Leu | Lys | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Glu | Tyr | Glu | Leu | Leu | Arg | Arg | Asn | Phe | Ser | Asp | Thr | Gly | Cys | Phe |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Gly | Phe | Gly | Ile | Gln | Glu | His | Ile | Asp | Leu | Gly | Ile | Lys | Tyr | Asp | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Thr | Gly | Ile | Tyr | Xaa | Met | Asp | Phe | Tyr | Val | Val | Leu | Glu | Arg | Ala |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Arg |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1288:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 137 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..137  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1288:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Glu | Lys | Lys | Gln | Ser | Asn | Pro | Met | Arg | Glu | Ile | Lys | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Lys | Leu | Val | Leu | Asn | Ile | Ser | Val | Gly | Glu | Ser | Gly | Asp | Arg | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Arg | Ala | Ala | Lys | Val | Leu | Glu | Gln | Leu | Ser | Gly | Gln | Ser | Pro | Val |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Phe | Ser | Lys | Ala | Arg | Tyr | Thr | Val | Arg | Ser | Phe | Gly | Ile | Arg | Arg | Asn |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Glu | Lys | Ile | Ala | Cys | Tyr | Val | Thr | Val | Arg | Gly | Glu | Lys | Ala | Met | Gln |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Leu | Glu | Ser | Gly | Leu | Lys | Val | Lys | Glu | Tyr | Glu | Leu | Leu | Arg | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asn | Phe | Ser | Asp | Thr | Gly | Cys | Phe | Gly | Phe | Gly | Ile | Gln | Glu | His | Ile |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Leu | Gly | Ile | Lys | Tyr | Asp | Pro | Ser | Thr | Gly | Ile | Tyr | Xaa | Met | Asp |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Phe | Tyr | Val | Val | Leu | Glu | Arg | Ala | Arg |     |     |     |     |     |     |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1289:

- (i) SEQUENCE CHARACTERISTICS:

09689980 101300

Thr Asp Gly Ile Cys Ile Xaa Val Pro Asp Cys Cys Ile Pro Val Ser  
1 5 10 15  
Ser Val Ser Phe Val Gly Ser Arg Xaa Arg Thr Arg Arg Met Ser Cys  
20 25 30

[illegible]

Cys Gly Gly Asn Cys Gly Xaa Gly Ala Gly Cys Lys Cys Gly Thr Ala  
35 40 45  
Ala Glu Gly Ala Arg Cys Thr Arg Thr Trp Leu Ser Arg  
50 55 60

(2) INFORMATION FOR SEQ ID NO:1292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1292:

Met Tyr Pro Asp Met Ala Glu Gln Val Thr Thr Thr Thr Gln Thr Leu  
1 5 10 15  
Ile Met Gly Val Ala Pro Ser Lys Gly Gly Phe Glu Ala Ala Xaa  
20 25 30  
Leu Arg Thr Ala Gly Ala Ser Xaa Ala Pro Thr Ala Pro Ala Thr Pro  
35 40 45  
Ala Pro Ala Ser Glu Thr Thr Ala Met Thr Xaa Gln Gly Val Asn Trp  
50 55 60  
Asp Arg Lys Asp Ser Phe Ile Leu Ser Ser Ser Ile Ile Phe  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1293:

Met Ala Glu Gln Val Thr Thr Thr Gln Thr Leu Ile Met Gly Val  
1 5 10 15  
Ala Pro Ser Lys Gly Gly Phe Glu Ala Ala Ala Xaa Leu Arg Thr Ala  
20 25 30  
Gly Ala Ser Xaa Ala Pro Thr Ala Pro Ala Thr Pro Ala Pro Ala Ser  
35 40 45  
Glu Thr Thr Ala Met Thr Xaa Gln Gly Val Asn Trp Asp Arg Lys Asp  
50 55 60  
Ser Phe Ile Leu Ser Ser Ser Ile Ile Phe  
65 70

(2) INFORMATION FOR SEQ ID NO:1294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..449
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1294:

gaagaggggaa ggggggatat cggggaaaaa aacacaaggt accagcagcg caaagagccg



(2) INFORMATION FOR SEQ ID NO:1295:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1597621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1295:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Glu | Gly | Arg | Gly | Asp | Ile | Gly | Glu | Lys | Asn | Thr | Arg | Tyr | Gln | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Lys | Glu | Pro | Gly | Val | Gly | Thr | Asp | Gln | Ala | Ala | Ala | Trp | Arg | Xaa |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Arg | Gly | Phe | Gly | Glu | Gln | Arg | Asp | His | Arg | Gly | Gly | Glu | Gln | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Glu | Pro | Arg | Asn | Gly | Gly | Ser | Ala | Arg | Trp | Leu | Pro | Ala | Ser | Cys |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Cys | Ser | Ser | Ser | Pro | Gly | Thr | Thr | Arg | Cys | Met | Cys | Thr | Arg | Arg | Arg |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Arg | Ser | Arg | Arg | Arg | Arg | Arg | Ser | Arg | Ser | Pro | Arg | Gly | Ser |     |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1296:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1597622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1296:

|          |     |     |     |          |     |     |     |     |           |     |     |     |     |           |     |
|----------|-----|-----|-----|----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|
| Lys<br>1 | Arg | Glu | Gly | Gly<br>5 | Ile | Ser | Gly | Lys | Lys<br>10 | Thr | Gln | Gly | Thr | Ser<br>15 | Ser |
| Ala      | Lys | Ser | Arg | Val      | Leu | Ala | Gln | Ile | Arg       | Arg | Pro | His | Gly | Asp       | Xaa |
|          |     |     | 20  |          |     |     | 25  |     |           |     |     | 30  |     |           |     |
| Phe      | Ala | Asp | Ser | Ala      | Asn | Asn | Val | Ile | Ile       | Glu | Glu | Val | Asn | Lys       | Gly |
|          |     | 35  |     |          |     |     | 40  |     |           |     |     | 45  |     |           |     |
| Leu      | Asn | Pro | Gly | Met      | Val | Val | Leu | Leu | Asp       | Gly | Cys | Gln | Leu | Pro       | Ala |
|          | 50  |     |     |          |     |     | 55  |     |           |     | 60  |     |     |           |     |
| Ala      | Leu | Leu | Arg | Arg      | Glu | Leu | Arg | Ala | Val       | Cys | Val | Arg | Ala | Glu       | Asp |
| 65       |     |     |     |          | 70  |     |     |     |           | 75  |     |     |     | 80        |     |
| Ala      | Pro | Ala | Glu | Glu      | Glu | Glu | Ala | Gly | Leu       | Gln | Glu | Glu | Ala | Glu       | Glu |
|          |     |     |     | 85       |     |     |     |     | 90        |     |     |     |     | 95        |     |
| Gly      | Lys | Ala | Glu | Ala      | Gly | Gly | Leu | Gly | Ala       | Arg | Gly | Val | Asn | Arg       | Gln |
|          |     | 100 |     |          |     |     |     | 105 |           |     |     |     | 110 |           |     |
| Gly      | Cys | Arg | Arg | Ser      | Ala | Arg | Pro | Glu | Pro       | Ala | Pro | Tyr | Leu | His       | Asp |
|          |     | 115 |     |          |     |     | 120 |     |           |     |     | 125 |     |           |     |
| Cys      | Arg | Arg | Lys | Lys      | Ile | His | Leu | Leu | Glu       | Pro | Arg | Cys | Ser |           |     |
|          | 130 |     |     |          |     | 135 |     |     |           |     | 140 |     |     |           |     |

[illegible]

(2) INFORMATION FOR SEQ ID NO:1297:

- ```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 90 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
    (A) NAME/KEY: peptide
    (B) LOCATION: 1..90
    (D) OTHER INFORMATION: / Ceres Seq. ID 1597623
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1297:

Met	Val	Val	Leu	Leu	Asp	Gly	Cys	Gln	Leu	Pro	Ala	Ala	Leu	Leu	Arg
1				5					10					15	
Arg	Glu	Leu	Arg	Ala	Val	Cys	Val	Arg	Ala	Glu	Asp	Ala	Pro	Ala	Glu
			20					25					30		
Glu	Glu	Glu	Ala	Gly	Leu	Gln	Glu	Glu	Ala	Glu	Glu	Gly	Lys	Ala	Glu
			35				40					45			
Ala	Gly	Gly	Leu	Gly	Ala	Arg	Gly	Val	Asn	Arg	Gln	Gly	Cys	Arg	Arg
	50					55					60				
Ser	Ala	Arg	Pro	Glu	Pro	Ala	Pro	Tyr	Leu	His	Asp	Cys	Arg	Arg	Lys
65					70					75					80
Lys	Ile	His	Leu	Leu	Glu	Pro	Arg	Cys	Ser						
				85					90						

(2) INFORMATION FOR SEQ ID NO:1298:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 385 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..385  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1298:

aatcaactcg	caatttcgcga	ttcgtttccaa	ctcctgagca	cttttctcctc	gtcccagaca	60
agccaatcga	agccgagata	cgaccatgga	ctccaccggc	accggagcag	ggggtaaggg	120
gaagaaggga	gcggccgggc	gcaaggtcgg	cgggccaagg	aagaagtcgg	tgtcgaggtc	180
cgtgaaggcc	ggtctccagt	tccccgtcgg	ccgcacccgg	cgctacttka	agaagggccg	240
ctacgcgcab	gttcggcacc	ggcgcccccg	tctacctcgc	cgctgtcttc	gaataacctcg	300
ccgtgaggt	tctggagctc	gccggtaatg	ctgccaggga	caacaagaag	actcgatta	360
ttccgcgccca	cgtgctttctk	gcgat				

(2) INFORMATION FOR SEQ ID NO:1299:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 38 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..38  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1299:

[illegible][illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..60

(D) OTHER INFORMATION: / Ceres Seq. ID 1597633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1300:

<div>(X1) SEQUENCE ALIGNMENT</div>															
Ser	Thr	Arg	Asn	Ser	Ala	Phe	Val	Pro	Thr	Pro	Glu	His	Phe	Leu	Leu
1				5					10					15	
Val	Pro	Asp	Lys	Pro	Ile	Glu	Ala	Glu	Ile	Arg	Pro	Trp	Thr	Pro	Pro
			20					25					30		
Ala	Pro	Glu	Gln	Gly	Val	Arg	Gly	Arg	Arg	Glu	Arg	Pro	Gly	Ala	Arg
			35				40					45			
Ser	Ala	Gly	Gln	Gly	Arg	Ser	Arg	Cys	Arg	Gly	Pro				
			50			55					60				

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..73

(D) OTHER INFORMATION: / Ceres Seq. ID 1597634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1301:

[illegible]

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 470 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..470

(D) OTHER INFORMATION: / Ceres Seq. ID 1597639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1302:

(X1)	SEQUENCE	DESCRIPTION	SIZE	ID	NO. OF	
aacaatgccca	attgccagca	accctatccat	acttttcagct	gttgatacaa	aaagagaaga	60
gagaatggcg	gavaacccag	agttgagtgg	tcttattact	caaacaaaga	agaaaaatat	120
agtgccaaag	ttcaccgaaa	tcttccccgt	ggaggacacg	cctaccctta	cagcgctctc	180
atcacctccg	tccggaaaga	agtgatcaaa	tactgcacca	accatacagg	catcgctccag	240
cccggtgctgc	cgctggagaa	gaatgtcccc	gagctctggg	tctacaccga	gctcaaaacg	300
aagaccaggt	ccatcacag	cgccatacgt	atggacaacc	tctacctggg	cggcttcagg	360
acccccggcg	gtgtgggtggg	agttcggcaa	ggacggcgac	accacctcc	tcgacgacaa	420

[illegible]

cgccaagtgg ctcggctttg gcgggccggt accaggacct catcgggcag

(2) INFORMATION FOR SEQ ID NO:1303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..67  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1303:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..66  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1304:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..69  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1305:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10

Met	Ser	Pro	Ser	Ser	Gly	Ser	Thr	Pro	Ser	Ser	Lys	Arg	Arg	Pro	Gly
1			5					10						15	
Pro	Ser	Arg	Ser	Pro	Tyr	Val	Trp	Thr	Thr	Ser	Thr	Trp	Ser	Ala	Ser
			20				25						30		

(2) INFORMATION FOR SEQ ID NO:1306:

(A) LENGTH: 371 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: sing

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

(ix) FEATURE:

## (7) NAME

(A) NAME/REF: \_\_\_\_\_  
(B) LOCATION: 1 \_\_\_\_\_

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:1306:

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:1900:  
agggaa ttgcacaaagc gatactagct agtccctacc aa

accaagga	ttcacaaagc	gatactagct	agtctctacc	aaagcattct	ctctgaadca	38
ctcttgcaat	ccactgagtt	ctgtttgttg	agacgcatag	agctagagtc	gacaatgtcg	120
ctctgtaggc	gcasaacgtg	ttcgaccctt	tctccatgga	cctctgggac	cccttcgaca	180
ccatgttccg	ctccatcgtc	ccgtcggcga	cctccaccaa	ctccgagact	gccgccttcg	240
ccagcgcccg	catcgactgg	aaggagacgc	ccgaggcgca	cgtgttcaag	gccgacctcc	300
ccggcgtcaa	gaaggaagag	gtcaaggctg	aggctcgagga	cggcaacatg	ctgggtcatca	360
cgggccagcg	c					

(2) INFORMATION FOR SEQ ID NO:1307:

(i) SEOUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino ac

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(ix) FEATURE:

```
(A) NAME/KEY: peptide
(B) LOCATION: 1..123
```

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:1307:

Lys Glu Ile His Lys Ala Ile Leu Ala Ser Pr

1				5				10				15			
Leu	Pro	Glu	Thr	Leu	Leu	Gln	Ser	Thr	Glu	Phe	Cys	Leu	Leu	Arg	Arg
			20					25					30		
Ile	Glu	Leu	Glu	Ser	Thr	Met	Ser	Leu	Val	Arg	Arg	Xaa	Thr	Cys	Ser
		35					40					45			
Thr	Pro	Ser	Pro	Trp	Thr	Ser	Gly	Thr	Pro	Ser	Thr	Pro	Cys	Ser	Ala
	50					55					60				
Pro	Ser	Ser	Arg	Arg	Arg	Pro	Pro	Pro	Thr	Pro	Arg	Leu	Pro	Pro	Ser
65					70					75				80	
Pro	Ala	Pro	Ala	Ser	Thr	Gly	Arg	Arg	Arg	Pro	Arg	Arg	Thr	Cys	Ser
				85					90					95	
Arg	Pro	Thr	Ser	Pro	Ala	Ser	Arg	Arg	Lys	Arg	Ser	Arg	Ser	Arg	Ser
			100					105					110		
Arg	Thr	Ala	Thr	Cys	Trp	Ser	Ser	Ala	Ser						
		115					120								

(2) INFORMATION FOR SEQ ID NO:1308:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

[illegible]

(A) NAME/KEY: peptide

(B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1597660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1308:

Met Ser Leu Val Arg Arg Xaa Thr Cys Ser Thr Pro Ser Pro Trp Thr  
1 5 10 15  
Ser Gly Thr Pro Ser Thr Pro Cys Ser Ala Pro Ser Ser Arg Arg Arg  
20 25 30  
Pro Pro Pro Thr Pro Arg Leu Pro Pro Ser Pro Ala Pro Ala Ser Thr  
35 40 45  
Gly Arg Arg Arg Pro Arg Arg Thr Cys Ser Arg Pro Thr Ser Pro Ala  
50 55 60  
Ser Arg Arg Lys Arg Ser Arg Ser Arg Ser Arg Thr Ala Thr Cys Trp  
65 70 75 80  
Ser Ser Ala Ala Ser  
85

(2) INFORMATION FOR SEQ ID NO:1309:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1597661

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1309:

Met Asp Leu Trp Asp Pro Phe Asp Thr Met Phe Arg Ser Ile Val Pro  
1 5 10 15  
Ser Ala Thr Ser Thr Asn Ser Glu Thr Ala Ala Phe Ala Ser Ala Arg  
20 25 30  
Ile Asp Trp Lys Glu Thr Pro Glu Ala His Val Phe Lys Ala Asp Leu  
35 40 45  
Pro Gly Val Lys Lys Glu Glu Val Lys Val Glu Val Glu Asp Gly Asn  
50 55 60  
Met Leu Val Ile Ser Gly Gln Arg  
65 70

(2) INFORMATION FOR SEQ ID NO:1310:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..236

(D) OTHER INFORMATION: / Ceres Seq. ID 1597666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1310:

acgcggaac cctagcagct caacaccctc gaggtacctc cattcgagct cggccgtgct 60  
ctcggagccg cgggagatgg cggatcagga gaccgtagct gtggttgagg caccaacccc 120  
ggttcctggg gaacgatgga cctgatgact gccctgcac tcgtcatgaa gaagtcaggt 180  
gctcacgatk gccttttgaa gggctctcgt gaggtgcc aagcatcgag aagcat

(2) INFORMATION FOR SEQ ID NO:1311:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..47

(D) OTHER INFORMATION: / Ceres Seq. ID 1597667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1311:

Arg Gly Asn Pro Ser Ser Ser Thr Pro Ser Arg Tyr Leu His Ser Gln  
1 5 10 15  
Ser Ala Val Ser Ser Glu Pro Arg Glu Met Ala Asp Gln Glu Thr Val  
20 25 30  
Ala Val Val Glu Ala Pro Thr Pro Val Leu Gly Glu Arg Trp Thr  
35 40 45

(2) INFORMATION FOR SEQ ID NO:1312:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..31

(D) OTHER INFORMATION: / Ceres Seq. ID 1597668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1312:

Ala Glu Thr Leu Ala Ala Gln His Pro Arg Gly Thr Ser Ile Arg Ser  
1 5 10 15  
Arg Pro Cys Pro Arg Ser Arg Gly Arg Trp Arg Ile Arg Arg Pro  
20 25 30

(2) INFORMATION FOR SEQ ID NO:1313:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..33

(D) OTHER INFORMATION: / Ceres Seq. ID 1597669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1313:

Met Asp Leu Met Thr Ala Leu Xaa Leu Val Met Lys Lys Ser Gly Ala  
1 5 10 15  
His Asp Xaa Leu Leu Lys Gly Leu Arg Glu Ala Ala Lys Ala Ser Arg  
20 25 30

Ser

(2) INFORMATION FOR SEQ ID NO:1314:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..401

(D) OTHER INFORMATION: / Ceres Seq. ID 1597674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1314:

ttctgaagtt tgcggcggcg cgtaggtagc ggcggtgtgc ttgtgatctc aatctcaacc	60
ccaggcgagc tgcggctccg tcacccgtcg atccacgcaa ccatgtcgag gaggaagacc	120
agggagccca aggaggagaa cgttaccctt ggaccactg tccgtgaagg agagtttgtb	180
tttggtgttg ctcatctt tgcattcctt aatgacacct tcattcatgt cactgatttg	240

tctgggaggg aaactttggt tcggatcact ggtggcatga aggttaaggc tgatcgtgat 300  
gagtcgtctc cttatgctgc tatgcttgct gcccaagatg ttgcacagcg ttgcaaggag 360  
ctcggatatca cagcgtgca cattaagctt cgtgccactg g

(2) INFORMATION FOR SEQ ID NO:1315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1315:

Met Ser Arg Arg Lys Thr Arg Glu Pro Lys Glu Glu Asn Val Thr Leu  
1 5 10 15  
Gly Pro Thr Val Arg Glu Gly Glu Phe Xaa Phe Gly Val Ala His Ile  
20 25 30  
Phe Ala Ser Phe Asn Asp Thr Phe Ile His Val Thr Asp Leu Ser Gly  
35 40 45  
Arg Glu Thr Leu Val Arg Ile Thr Gly Gly Met Lys Val Lys Ala Asp  
50 55 60  
Arg Asp Glu Ser Ser Pro Tyr Ala Ala Met Leu Ala Ala Gln Asp Val  
65 70 75 80  
Ala Gln Arg Cys Lys Glu Leu Gly Ile Thr Ala Leu His Ile Lys Leu  
85 90 95  
Arg Ala Thr

(2) INFORMATION FOR SEQ ID NO:1316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..399
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1316:

catcaatagc cagttctaatt ctcaggttrg gggaaatagg cctcgcgggt cgcaaaccgc 60  
tctctgctga ttttggattt cggaggcgct cgagttttca ggtaaactat agtttagtga 120  
cccatggctc gtactaagca aactgctcgc aagtccactg gaggaaggc tccwaggaaa 180  
caacttgcca ccaaggctgc ccgtaagtct gcacctacaa ctgggggagt aaagaagcct 240  
caccgttacc gccctggaac tggtgctctt cgtgaaatcc gcaagtatca gaagagcact 300  
gacctgctca taaggaagct tccgttccaa aggcttgatc gggagattkc ccaggatttc 360  
aagactgata ttcgtttcca gagccatgag gtgcttgag

(2) INFORMATION FOR SEQ ID NO:1317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597699

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1317:

Met Ala Arg Thr Lys Gln Thr Ala Arg Lys Ser Thr Gly Gly Lys Ala

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1 5 10 15  
Xaa Arg Lys Gln Leu Ala Thr Lys Ala Arg Lys Ser Ala Pro Thr  
20 25 30  
Thr Gly Gly Val Lys Lys Pro His Arg Tyr Arg Pro Gly Thr Val Ala  
35 40 45  
Leu Arg Glu Ile Arg Lys Tyr Gln Lys Ser Thr Asp Leu Leu Ile Arg  
50 55 60  
Lys Leu Pro Phe Gln Arg Leu Val Arg Glu Ile Xaa Gln Asp Phe Lys  
65 70 75 80  
Thr Asp Leu Arg Phe Gln Ser His Ala Val Leu Ala  
85 90

(2) INFORMATION FOR SEQ ID NO:1318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..493
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1318:

gaaggcatct ccaatctcct cgccccccac ggacctgaac cgagaaccgt taccgccgcc 60  
gcctctcgcc tagccgccgg agaagcgccg ctgcgtcagg aggacagcca tggcgccgga 120  
gccggagatg atattatgaa cgagaagaat ccccgcccgc tcgacgagga tracatcgcg 180  
ctcctcaaaa cctatggact gggggccgtat tcgaccagca ttaagaaggt cgagaaggag 240  
atcaaggaaa tggccaagaa aatcaacgac ctctgtggga taaaggagtc tgatacaggg 300  
ctggctccac ctagccagtg ggatttggtt tcagataagc agatgatgca agaagaacaa 360  
ccgttacaag tagcaagatg tacaagatt ataagcccta atacggatga tgccaaatat 420  
gttataaatg traacaaat tgcaaagttt gtggtcggat tgggagataa ggtctctcca 480  
actgatatcg agg

(2) INFORMATION FOR SEQ ID NO:1319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597727

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1319:

Glu Gly Ile Ser Asn Leu Leu Ala Pro His Gly Pro Glu Pro Arg Thr  
1 5 10 15  
Val Thr Ala Ala Ala Ser Arg Leu Ala Ala Gly Glu Ala Pro Leu Ala  
20 25 30  
Gln Glu Asp Ser His Gly Ala Gly Ala Gly Asp Asp Ile Met Asn Glu  
35 40 45  
Lys Asn Pro Arg Pro Leu Asp Glu Asp Xaa Ile Ala Leu Leu Lys Thr  
50 55 60  
Tyr Gly Leu Gly Pro Tyr Ser Thr Ser Ile Lys Lys Val Glu Lys Glu  
65 70 75 80  
Ile Lys Glu Met Ala Lys Lys Ile Asn Asp Leu Cys Gly Ile Lys Glu  
85 90 95  
Ser Asp Thr Gly Leu Ala Pro Pro Ser Gln Trp Asp Leu Val Ser Asp  
100 105 110  
Lys Gln Met Met Gln Glu Glu Gln Pro Leu Gln Val Ala Arg Cys Thr  
115 120 125  
Lys Ile Ile Ser Pro Asn Thr Asp Asp Ala Lys Tyr Val Ile Asn Xaa

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130 135 140  
Lys Gln Ile Ala Lys Phe Val Val Gly Leu Gly Asp Lys Val Ser Pro  
145 150 155 160  
Thr Asp Ile Glu

(2) INFORMATION FOR SEQ ID NO:1320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1320:

Met Asn Glu Lys Asn Pro Arg Pro Leu Asp Glu Asp Xaa Ile Ala Leu  
1 5 10 15  
Leu Lys Thr Tyr Gly Leu Gly Pro Tyr Ser Thr Ser Ile Lys Lys Val  
20 25 30  
Glu Lys Glu Ile Lys Glu Met Ala Lys Lys Ile Asn Asp Leu Cys Gly  
35 40 45  
Ile Lys Glu Ser Asp Thr Gly Leu Ala Pro Pro Ser Gln Trp Asp Leu  
50 55 60  
Val Ser Asp Lys Gln Met Met Gln Glu Glu Gln Pro Leu Gln Val Ala  
65 70 75 80  
Arg Cys Thr Lys Ile Ile Ser Pro Asn Thr Asp Asp Ala Lys Tyr Val  
85 90 95  
Ile Asn Xaa Lys Gln Ile Ala Lys Phe Val Val Gly Leu Gly Asp Lys  
100 105 110  
Val Ser Pro Thr Asp Ile Glu  
115

(2) INFORMATION FOR SEQ ID NO:1321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..425
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1321:

caatgagttg aggagagtgg aacatgttga ccattctaga aagtytgcag agcargctgt 60  
aaaggcgatc aagggcaaag agtccggtga accagttccg gagtatgact acctgccata 120  
cttctactcc cgatcattcg acctggcgtg gcaattotac ggcgacaacg tgggcgaaac 180  
tattctgttt ggcgacagtg accccacctc cagcaagccc aagttcggct cgtactggat 240  
caaggacggc aaggtcttgg gcgccttccct ggagggcggg tcaccggacg agaacaaggc 300  
cattgccaaag gtggcgaaaaa cccagccgcc ggtoctaac ctcgaggagc tcaagaaggm 360  
tggcctccag ttcgccagca agatctgaga cgstcccgtt ccatgtaaat ttccgtgtca 420  
tcgtg

(2) INFORMATION FOR SEQ ID NO:1322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION: / Ceres Seq. ID 1597733

Asn	Glu	Leu	Arg	Arg	Val	Glu	His	Val	Asp	His	Ser	Arg	Lys	Xaa	Ala
1				5					10					15	
Glu	Xaa	Ala	Val	Lys	Ala	Ile	Lys	Gly	Lys	Glu	Ser	Gly	Glu	Pro	Val
			20					25					30		
Pro	Glu	Tyr	Asp	Tyr	Leu	Pro	Tyr	Phe	Tyr	Ser	Arg	Ser	Phe	Asp	Leu
			35				40					45			
Ala	Trp	Gln	Phe	Tyr	Gly	Asp	Asn	Val	Gly	Glu	Thr	Ile	Leu	Phe	Gly
	50					55					60				
Asp	Ser	Asp	Pro	Thr	Ser	Ser	Lys	Pro	Lys	Phe	Gly	Ser	Tyr	Trp	Ile
65				70						75				80	
Lys	Asp	Gly	Lys	Val	Leu	Gly	Ala	Phe	Leu	Glu	Gly	Gly	Ser	Pro	Asp
				85					90					95	
Glu	Asn	Lys	Ala	Ile	Ala	Lys	Val	Ala	Lys	Thr	Gln	Pro	Pro	Val	Ala
			100					105					110		
Asn	Leu	Glu	Glu	Leu	Lys	Lys	Xaa	Gly	Leu	Gln	Phe	Ala	Ser	Lys	Ile
			115				120					125			

Met	Thr	Thr	Cys	His	Thr	Ser	Thr	Pro	Asp	His	Ser	Thr	Trp	Arg	Gly
1				5					10					15	
Asn	Ser	Thr	Ala	Thr	Thr	Trp	Ala	Lys	Leu	Ser	Cys	Leu	Ala	Thr	Val
			20					25					30		
Thr	Pro	Pro	Pro	Ala	Ser	Pro	Ser	Ser	Ala	Arg	Thr	Gly	Ser	Arg	Thr
			35				40					45			
Ala	Arg	Ser	Trp	Ala	Pro	Ser	Trp	Arg	Ala	Gly	His	Arg	Thr	Arg	Thr
	50					55					60				
Arg	Pro	Leu	Pro	Arg	Trp	Arg	Lys	Pro	Ser	Arg	Arg	Ser	Leu	Thr	Ser
65					70					75					80
Arg	Ser	Ser	Arg	Arg	Xaa	Ala	Ser	Ser	Ser	Pro	Ala	Arg	Ser	Glu	Thr
				85					90					95	
Xaa	Pro	Phe	His	Val	Asn	Phe	Arg	Val	Ile	Val					
			100					105							

(D) OTHER INFORMATION: / Ceres Seq. ID 1597741

ataaaaccct actaaccgcg tctcctctcc agcgcccgcc gtcgccgccg ccctcctctt

[illegible]

gggtcccgccg tccgtcgagg tcatcatggt gagggtcagt gtgctcaacg atgcgctcaa 120  
gtccatgtac aatgcagaga agaggggcaa gaggcaggtc atgatcaggc cgctcgccaa 180  
ggtgatcatc aagttcctga cggtcattga gcgtcatgga tacattggcg agttcgagta 240  
cgtggatgac cacagagctg ggaagattgt ggtggaactg aacggcagac taaacaaatg 300  
cgggtgtaatt agcccccggt ttgatgttgg ggtaaaggaa atcgaaggct ggactgcgag 360  
gctgcttccg tctcgccagt ttggctatat cgtgcttaca acctctgcgg gaattatgga 420  
tcacgaggag

(2) INFORMATION FOR SEQ ID NO:1325:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1597742

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1325:

Met Val Arg Val Ser Val Leu Asn Asp Ala Leu Lys Ser Met Tyr Asn  
1 5 10 15  
Ala Glu Lys Arg Gly Lys Arg Gln Val Met Ile Arg Pro Ser Ser Lys  
20 25 30  
Val Ile Ile Lys Phe Leu Thr Val Met Gln Arg His Gly Tyr Ile Gly  
35 40 45  
Glu Phe Glu Tyr Val Asp Asp His Arg Ala Gly Lys Ile Val Val Glu  
50 55 60  
Leu Asn Gly Arg Leu Asn Lys Cys Gly Val Ile Ser Pro Arg Phe Asp  
65 70 75 80  
Val Gly Val Lys Glu Ile Glu Gly Trp Thr Ala Arg Leu Leu Pro Ser  
85 90 95  
Arg Gln Phe Gly Tyr Ile Val Leu Thr Thr Ser Ala Gly Ile Met Asp  
100 105 110  
His Glu Glu  
115

(2) INFORMATION FOR SEQ ID NO:1326:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1597743

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1326:

Met Tyr Asn Ala Glu Lys Arg Gly Lys Arg Gln Val Met Ile Arg Pro  
1 5 10 15  
Ser Ser Lys Val Ile Ile Lys Phe Leu Thr Val Met Gln Arg His Gly  
20 25 30  
Tyr Ile Gly Glu Phe Glu Tyr Val Asp Asp His Arg Ala Gly Lys Ile  
35 40 45  
Val Val Glu Leu Asn Gly Arg Leu Asn Lys Cys Gly Val Ile Ser Pro  
50 55 60  
Arg Phe Asp Val Gly Val Lys Glu Ile Glu Gly Trp Thr Ala Arg Leu  
65 70 75 80  
Leu Pro Ser Arg Gln Phe Gly Tyr Ile Val Leu Thr Thr Ser Ala Gly  
85 90 95  
Ile Met Asp His Glu Glu  
100

0066980 "101300

(2) INFORMATION FOR SEQ ID NO:1327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:

Met Ile Arg Pro Ser Ser Lys Val Ile Ile Lys Phe Leu Thr Val Met  
1 5 10 15  
Gln Arg His Gly Tyr Ile Gly Glu Phe Glu Tyr Val Asp Asp His Arg  
20 25 30  
Ala Gly Lys Ile Val Val Glu Leu Asn Gly Arg Leu Asn Lys Cys Gly  
35 40 45  
Val Ile Ser Pro Arg Phe Asp Val Gly Val Lys Glu Ile Glu Gly Trp  
50 55 60  
Thr Ala Arg Leu Leu Pro Ser Arg Gln Phe Gly Tyr Ile Val Leu Thr  
65 70 75 80  
Thr Ser Ala Gly Ile Met Asp His Glu Glu  
85 90

(2) INFORMATION FOR SEQ ID NO:1328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..378
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1328:

atcccacttc cacccaaata caccaccgcc ataccagcgt gtccgcgatt ccgtcgagtt 60  
agaccagtcg agagagcagt ccagagcgag aagaggtgaa tatgagttcc ggcggcggca 120  
ggggcaagcc caaggggtcc aaggctgtgt cgcggtcgac caaggctggg ctgcagttcc 180  
ccgtcggcgc catcgcgcgc tacctcaagg cgggcaagta cgccgagcgc gtcggcgggtg 240  
gtgcgcccgt ctacctctcc gccgtcctcg agtatctcgc ggcagaggtg ttggaactgg 300  
cgggcaacgc ggcgcgcgac aacaagaaga accgcatcgt gccgcgccac atccagctcg 360  
ccgtgcgcaa cgacgagg

(2) INFORMATION FOR SEQ ID NO:1329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1329:

Ser His Phe His Pro Asn Pro Pro Pro Tyr Gln Arg Val Arg Asp  
1 5 10 15  
Ser Val Glu Leu Asp Gln Ser Arg Glu Gln Ser Gln Thr Arg Arg Gly  
20 25 30  
Glu Tyr Glu Phe Arg Arg Arg Gln Gly Gln Ala Gln Gly Val Gln Gly  
35 40 45

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Cys Val Ala Val Asp Gln Gly Trp Ala Ala Val Pro Arg Arg Pro His  
50 55 60  
Arg Ala Leu Pro Gln Gly Gly Gln Val Arg Arg Ala Arg Arg Arg Trp  
65 70 75 80  
Cys Ala Arg Leu Pro Leu Arg Arg Pro Arg Val Ser Arg Gly Arg Gly  
85 90 95  
Val Gly Thr Gly Gly Gln Arg Gly Ala Arg Gln Gln Glu Glu Pro His  
100 105 110  
Arg Ala Ala Pro His Pro Ala Arg Arg Ala Gln Arg Arg  
115 120 125

(2) INFORMATION FOR SEQ ID NO:1330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1330:

Met Ser Ser Gly Gly Gly Arg Gly Lys Pro Lys Gly Ser Lys Ala Val  
1 5 10 15  
Ser Arg Ser Thr Lys Ala Gly Leu Gln Phe Pro Val Gly Arg Ile Ala  
20 25 30  
Arg Tyr Leu Lys Ala Gly Lys Tyr Ala Glu Arg Val Gly Gly Gly Ala  
35 40 45  
Pro Val Tyr Leu Ser Ala Val Leu Glu Tyr Leu Ala Ala Glu Val Leu  
50 55 60  
Glu Leu Ala Gly Asn Ala Ala Arg Asp Asn Lys Lys Asn Arg Ile Val  
65 70 75 80  
Pro Arg His Ile Gln Leu Ala Val Arg Asn Asp Glu  
85 90

(2) INFORMATION FOR SEQ ID NO:1331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..456
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1331:

ctctagaacc ctagcgcbnc gccggtcctg ccgcccgcgc agccgccatc gcacggccat	60
gggtatcgat ctcgtagccg gcggccgcaa caagaakacc aagcgcacgg cgcccaagtc	120
cgacgatgtc tacctcaagc tctcgtcaa gctctaccgc ttccttgtgc gcaggacaaa	180
gagcaacttc aacgccgtga tctcaagcg cctcttcattg agcaagacca accgcccgcc	240
gctctcggat gcgcccgcctc gtcagggttca tggaggggaa gggatgatcag atcgccgtga	300
ttgtgggcac cgtgaccgac gacaagagga tcagcgaggt gccggcgatg aaggtctgcg	360
cgctcagggt cactgagaca gcgagggccca ggatcatcaa tgctggcgga gagtgcctca	420
ccttcgacca gctcgcgctc cgtgccccac ttgggc	

(2) INFORMATION FOR SEQ ID NO:1332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(D) OTHER INFORMATION: / Ceres Seq. ID 1597749

[illegible][illegible]

(2) INFORMATION FOR SEQ ID NO:1335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..294
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1335:

gttgttttgt tcttgcggaacgagacgag actaggcgac gcgasgtyag ggagtcgagg	60
aggatcgagg ctcaggcaag atgaacagga agccaggaga ctgggactgc agggcggtgcc	120
ancacctcaa cttcagccgc cgagacatat gccagckctg tagcgagcca cgtggagttg	180
ctgatcggtg cagtggcggc ggcggaggag gaggaggagg cgactacgca agctttcggt	240
ggccgcggtg gctcctcctt cggcgcggc tttgggcgct gctggctctg acgt	

(2) INFORMATION FOR SEQ ID NO:1336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1336:

Leu Phe Cys Ser Cys Gly Asn Glu Thr Arg Leu Gly Asp Ala Xaa Xaa	
1 5 10 15	
Gly Ser Arg Gly Gly Ser Gly Leu Arg Gln Asp Glu Gln Glu Ala Arg	
20 25 30	
Arg Leu Gly Leu Gln Gly Val Pro Xaa Pro Gln Leu Gln Pro Pro Arg	
35 40 45	
His Met Pro Xaa Leu	
50	

(2) INFORMATION FOR SEQ ID NO:1337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1337:

Met Asn Arg Lys Pro Gly Asp Trp Asp Cys Arg Ala Cys Xaa His Leu	
1 5 10 15	
Asn Phe Ser Arg Arg Asp Ile Cys Gln Xaa Cys Ser Glu Pro Arg Gly	
20 25 30	
Val Ala Asp Arg Gly Ser Gly Gly Gly Gly Gly Gly Gly Asp	
35 40 45	
Tyr Ala Ser Phe Arg Trp Pro Arg Trp Leu Leu Leu Arg Arg Arg Leu	
50 55 60	
Trp Ala Leu Leu Ala Leu Thr	
65 70	

(2) INFORMATION FOR SEQ ID NO:1338:

(i) SEQUENCE CHARACTERISTICS:

09669900 "08669960



```

      (A) LENGTH: 442 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
      (A) NAME/KEY: -
      (B) LOCATION: 1..442
      (D) OTHER INFORMATION: / Ceres Seq. ID 1597755
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1338:

```

cttttaacct	cgcgcgcgca	tccgacgccc	atctgctcca	ccctccaccc	agccgcccgc	60
gccgcgcgct	aaggagaaga	gggtccggcc	gtctccttgc	cccgatggcg	tccgagaaga	120
agcagtccaa	cccgatgcgg	gagatcaagg	tgcagaagct	ggtcctcaac	atatccgtag	180
ggagagcggc	gaccgcctca	cccgcgccgc	caaggtgctg	gagcagctca	gcgccagacc	240
cccgctcttct	ccaaggcgag	gtacacgggtg	cgctcgttcg	gcatacggcg	taacgagaag	300
atcgcttgct	acgtcacggt	caggggcgac	aaggccatgc	agctgcttga	gagcggcctc	360
aaggtcaagg	agtcacagct	gctcaggagg	aacttcagcg	acaccggctg	cttcgggttc	420
qgcatccagg	agcacatcga	cc				

(2) INFORMATION FOR SEQ ID NO:1339:

```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 96 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
    (A) NAME/KEY: peptide
    (B) LOCATION: 1..96
    (D) OTHER INFORMATION: / Ceres Seq. ID 1597756
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1339:															
Phe	Asn	Leu	Ala	Pro	Pro	Ser	Asp	Ala	His	Leu	Leu	His	Pro	Pro	Pro
1				5				10					15		
Ser	Arg	Arg	Arg	Arg	Arg	Leu	Arg	Arg	Arg	Gly	Ser	Gly	Arg	Leu	Leu
			20					25					30		
Ala	Pro	Met	Ala	Ser	Glu	Lys	Lys	Gln	Ser	Asn	Pro	Met	Arg	Glu	Ile
		35					40					45			
Lys	Val	Gln	Lys	Leu	Val	Leu	Asn	Ile	Ser	Val	Gly	Arg	Ala	Ala	Thr
	50					55					60				
Ala	Ser	Pro	Ala	Pro	Pro	Arg	Cys	Trp	Ser	Ser	Ser	Ala	Pro	Asp	Pro
65				70					75				80		
Arg	Leu	Leu	Gln	Gly	Glu	Val	His	Gly	Ala	Leu	Val	Arg	His	Pro	Ala
			85						90				95		

(2) INFORMATION FOR SEQ ID NO:1340:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 62 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..62
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1597757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1340:															
Met	Ala	Ser	Glu	Lys	Lys	Gln	Ser	Asn	Pro	Met	Arg	Glu	Ile	Lys	Val
1				5					10					15	
Gln	Lys	Leu	Val	Leu	Asn	Ile	Ser	Val	Gly	Arg	Ala	Ala	Thr	Ala	Ser
			20					25					30		
Pro	Ala	Pro	Pro	Arg	Cys	Trp	Ser	Ser	Ser	Ala	Pro	Asp	Pro	Arg	Leu

[illegible]

(2) INFORMATION FOR SEQ ID NO:1341:

(A) LENGTH: 52 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..52

(D) OTHER INFORMATION: / Ceres Seq. ID 1597758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1341:

Met Arg Glu Ile Lys Val Gln Lys Leu Val Leu Asn Ile Ser Val Gly  
1 5 10 15  
Arg Ala Ala Thr Ala Ser Pro Ala Pro Pro Arg Cys Trp Ser Ser Ser  
20 25 30  
Ala Pro Asp Pro Arg Leu Leu Gln Gly Glu Val His Gly Ala Leu Val  
35 40 45  
Arg His Pro Ala  
50

(2) INFORMATION FOR SEQ ID NO:1342:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 422 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..422

(D) OTHER INFORMATION: / Ceres Seq. ID 1597797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1342:

Sequence 15 (NR_115127)						
atcgccccgc	gaaccctagc	tccgcgaact	gccgcgcgcca	ctcccacgct	cgcagccatg	60
ccgcccgaagc	tcgacccgtc	gcaggtggtg	gaggtgttcg	tccgtgtgac	cggcggcgag	120
gtcggcgcac	gtcttcgctg	gcccccaaga	tcggcccgcct	cggctctttcc	cccaagaaga	180
tcggagagga	catcgccaag	gagacggcca	aggactggaa	gggcctccgc	gtcacccgtca	240
agctcacccgt	ccagaaccgg	cagccaaggt	ctccgtcgtc	ccctccgccg	cggcgctcgt	300
catcaaggcg	ctcaaggagc	cagagaggga	ccgcaagaag	gtcaagaaca	tcaagcacag	360
cgnaacatc	agcctcgacg	acgtcatcga	gatcgccagg	accatgaggc	acaggtccat	420
gg						

(2) INFORMATION FOR SEQ ID NO:1343:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1597798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1343:

Ile Ala Pro Arg Thr Leu Ala Pro Ala Thr Ala Ala Ala Thr Pro Thr  
1 5 10 15  
Leu Ala Ala Met Pro Pro Lys Leu Asp Pro Ser Gln Val Val Glu Val  
20 25 30  
Phe Val Arg Val Thr Gly Gly Glu Val Gly Ala Arg Leu Arg Trp Pro  
35 40 45

[illegible]

Met	Pro	Pro	Lys	Leu	Asp	Pro	Ser	Gln	Val	Val	Glu	Val	Phe	Val	Arg
1				5					10					15	
Val	Thr	Gly	Gly	Glu	Val	Gly	Ala	Arg	Leu	Arg	Trp	Pro	Pro	Arg	Ser
		20						25					30		
Ala	Arg	Ser	Val	Phe	Pro	Pro	Arg	Arg	Ser	Glu	Arg	Thr	Ser	Pro	Arg
		35					40					45			
Arg	Arg	Pro	Arg	Thr	Gly	Arg	Ala	Ser	Ala	Ser	Pro	Ser	Ser	Ser	Pro

[illegible]

145

150

(2) INFORMATION FOR SEQ ID NO:1348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1348:

Met	Val	Arg	Val	Ser	Val	Leu	Asn	Asp	Ala	Leu	Lys	Ser	Met	Tyr	Asn
1				5					10					15	
Ala	Glu	Lys	Ile	Gly	Lys	Arg	Gln	Val	Met	Ile	Arg	Pro	Ser	Ser	Lys
			20					25					30		
Val	Ile	Ile	Lys	Phe	Leu	Thr	Val	Met	Gln	Arg	His	Gly	Tyr	Ile	Gly
		35					40					45			
Glu	Phe	Glu	Tyr	Val	Asp	Asp	His	Arg	Ser	Gly	Lys	Ile	Val	Val	Glu
	50					55					60				
Leu	Asn	Gly	Arg	Leu	Asn	Lys	Cys	Gly	Val	Ile	Ser	Pro	Arg	Phe	Asp
65					70				75						80
Ile	Gly	Val	Lys	Asp	Ile	Glu	Gly	Trp	Thr	Ala	Ser	Cys	Ser	Arg	Pro
			85					90						95	
Gly	Ser	Ser	Asp	Thr	Ser	Ser	Ser	Gln	Leu	Arg	Gln	Ala	Ser	Trp	Thr
			100					105						110	
Thr	Arg	Arg	Pro	Ala	Gly	Arg	Ala								
			115				120								

(2) INFORMATION FOR SEQ ID NO:1349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597808

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1349:

Met	Tyr	Asn	Ala	Glu	Lys	Ile	Gly	Lys	Arg	Gln	Val	Met	Ile	Arg	Pro
1				5					10					15	
Ser	Ser	Lys	Val	Ile	Ile	Lys	Phe	Leu	Thr	Val	Met	Gln	Arg	His	Gly
			20					25					30		
Tyr	Ile	Gly	Glu	Phe	Glu	Tyr	Val	Asp	Asp	His	Arg	Ser	Gly	Lys	Ile
		35					40					45			
Val	Val	Glu	Leu	Asn	Gly	Arg	Leu	Asn	Lys	Cys	Gly	Val	Ile	Ser	Pro
	50					55					60				
Arg	Phe	Asp	Ile	Gly	Val	Lys	Asp	Ile	Glu	Gly	Trp	Thr	Ala	Ser	Cys
65					70				75						80
Ser	Arg	Pro	Gly	Ser	Ser	Asp	Thr	Ser	Ser	Gln	Leu	Arg	Gln	Ala	
			85					90						95	
Ser	Trp	Thr	Thr	Arg	Arg	Pro	Ala	Gly	Arg	Ala					
			100					105							

(2) INFORMATION FOR SEQ ID NO:1350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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